

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT: Daggett, Lorrie P.

Ellis, Steven B.

Liaw, Chen W.

Lu, Chin-Chun

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(ii) TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
SUBUNITS, DNA ENCODING SAME AND USES THEREFOR

(iii) NUMBER OF SEQUENCES: 21

15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark

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(C) CITY: Los Angeles

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(D) STATE: CA

(E) COUNTRY: U.S.A.

(F) ZIP: 90071-2921

(v) COMPUTER READABLE FORM:

25

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: 20-APR-1994

(C) CLASSIFICATION:

35

(vii) PRIOR APPLICATION DATA:

SD9383

(A) APPLICATION NUMBER: US 08/052,449

(B) FILING DATE: 20-APR-1993

(viii) ATTORNEY/AGENT INFORMATION:

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(A) NAME: Reiter, Stephen E.

(B) REGISTRATION NUMBER: 31,192

(C) REFERENCE/DOCKET NUMBER: P41 9424

(ix) TELECOMMUNICATION INFORMATION:

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(A) TELEPHONE: 619-546-4737

(B) TELEFAX: 619-546-9392

(2) INFORMATION FOR SEQ ID NO:1:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4298 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

20

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

25

(A) NAME/KEY: CDS

(B) LOCATION: 262..3078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

30

CAAGCCGGGC GTTCGGAGCT GTGCCCGGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG 60

CGTGGGGCTG AGCGCCGAGC CCCC CGCAC GCTTCAGCCC CCC'TCCCTC GGCCGACGTC 120

CCGGGACCGC CGCTCCGGG GAGACGTGGC GTCCGAGCC CGCGGGGCCG GGCGAGCGCA 180

35

GGACGGCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG 240

CCAGGCCCCGC GGGCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC 291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala
5 1 5 10

CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC 339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile
15 20 25

10 GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC 387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe
30 35 40

15 CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT 435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile
45 50 55

20 CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG 483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met
60 65 70

GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC 531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile
25 75 80 85 90

CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT 579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro
95 100 105

30 GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC 627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr
110 115 120

35 ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG 675

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	Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	
	125 130 135	
5	CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG	723
	Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	
	140 145 150	
10	ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC	771
	Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	
	155 160 165 170	
15	CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG	819
	His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	
	175 180 185	
	CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG	867
	Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys	
	190 195 200	
20	AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC	915
	Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val	
	205 210 215	
25	ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC ACT GTA TAC CGC GCA	963
	Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala	
	220 225 230	
30	GCC GCG ATG CTG AAC ATG ACG GGC TCC GGG TAC GTG TGG CTG GTC GGC	1011
	Ala Ala Met Leu Asn Met Thr Gly Ser Gly Tyr Val Trp Leu Val Gly	
	235 240 245 250	
35	GAG CGC GAG ATC TCG GGG AAC GCC CTG CGC TAC GCC CCA GAC GGC ATC	1059
	Glu Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile	
	255 260 265	

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	CTC GGG CTG CAG CTC ATC AAC GGC AAG AAC GAG TCG GCC CAC ATC AGC	1107
	Leu Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu Ser Ala His Ile Ser	
	270 275 280	
5	GAC GCC GTG GGC GTG GTG GCC CAG GCC GTG CAC GAG CTC CTC GAG AAG	1155
	Asp Ala Val Gly Val Val Ala Gln Ala Val His Glu Leu Leu Glu Lys	
	285 290 295	
	GAG AAC ATC ACC GAC CCG CCG CGG GGC TGC GTG GGC AAC ACC AAC ATC	1203
10	Glu Asn Ile Thr Asp Pro Pro Arg Gly Cys Val Gly Asn Thr Asn Ile	
	300 305 310	
	TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG TAT	1251
	Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr	
15	315 320 325 330	
	GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT GAG GAT GGG GAC CGG	1299
	Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg	
	335 340 345	
20	AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG GTG	1347
	Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val	
	350 355 360	
25	CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG AAG	1395
	Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys	
	365 370 375	
	ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG ATG	1443
30	Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met	
	380 385 390	
	TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG TAC	1491
	Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr	
35	395 400 405 410	

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	GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG GAG GAG TTC ACA GTC	1539
	Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val	
	415 420 425	
5	AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC ACG	1587
	Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr	
	430 435 440	
10	TCG CCG GGC AGC CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC TTT	1635
	Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe	
	445 450 455	
	TGC ATC GAC CTG CTC ATC AAG CTG GCA CGG ACC ATG AAC TTC ACC TAC	1683
15	Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr	
	460 465 470	
	GAG GTG CAC CTG GTG GCA GAT GGC AAG TTC GGC ACA CAG GAG CGG GTG	1731
	Glu Val His Leu Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val	
20	475 480 485 490	
	AAC AAC AGC AAC AAG AAG GAG TGG AAT GGG ATG ATG GGC GAG CTG CTC	1779
	Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu	
	495 500 505	
25	AGC GGC CAG GCA GAC ATG ATC GTG GCG CCG CTA ACC ATA AAC AAC GAG	1827
	Ser Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu	
	510 515 520	
30	CGC GCG CAG TAC ATC GAG TTT TCC AAG CCC TTC AAG TAC CAG GGC CTG	1875
	Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu	
	525 530 535	
	ACT ATT CTG GTC AAG AAG GAG ATT CCC CGG AGC ACG CTG GAC TCG TTC	1923
35	Thr Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe	

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	540	545	550	
	ATG CAG CCG TTC CAG AGC ACA CTG TGG CTG CTG GTG GGG CTG TCG GTG 1971			
	Met Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val			
5	555	560	565	570
	CAC GTG GTG GCC GTG ATG CTG TAC CTG CTG GAC CGC TTC AGC CCC TTC 2019			
	His Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe			
	575	580	585	
10	GGC CGG TTC AAG GTG AAC AGC GAG GAG GAG GAG GAG GAC GCA CTG ACC 2067			
	Gly Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Glu Asp Ala Leu Thr			
	590	595	600	
15	CTG TCC TCG GCC ATG TGG TTC TCC TGG GGC GTC CTG CTC AAC TCC GGC 2115			
	Leu Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly			
	605	610	615	
	ATC GGG GAA GGC GCC CCC AGA AGC TTC TCA GCG CGC ATC CTG GGC ATG 2163			
20	Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met			
	620	625	630	
	GTG TGG GCC GGC TTT GCC ATG ATC ATC GTG GCC TCC TAC ACC GCC AAC 2211			
	Val Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn			
25	635	640	645	650
	CTG GCG GCC TTC CTG GTG CTG GAC CGG CCG GAG GAG CGC ATC ACG GGC 2259			
	Leu Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly			
	655	660	665	
30	ATC AAC GAC CCT CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC GCC 2307			
	Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala			
	670	675	680	
35	ACG GTG AAG CAG AGC TCC GTG GAT ATC TAC TTC CGG CGC CAG GTG GAG 2355			

Thr Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu
685 690 695

CTG AGC ACC ATG TAC CGG CAT ATG GAG AAG CAC AAC TAC GAG AGT GCG 2403
5 Leu Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala
700 705 710

GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC ATC 2451
Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile
10 715 720 725 730

TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC CTG 2499
Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu
735 740 745

15 GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC ATG 2547
Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met
750 755 760

20 CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG 2595
Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys
765 770 775

TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG 2643
25 Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg
780 785 790

TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT 2691
Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe
30 795 800 805 810

GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC 2739
Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala
815 820 825

35

GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT 2787
 Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp
 830 835 840

5 GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG TGG 2835
 Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp
 845 850 855

10 CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT 2883
 Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro
 860 865 870

15 AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC 2931
 Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser
 875 880 885 890

TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG AGC ACC GGG GGT GGA CGC 2979
 Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Ser Thr Gly Gly Gly Arg
 895 900 905

20 GGT GCT TTG CAA AAC CAA AAA GAC ACA GTG CTG CCG CGA CGC GCT ATT 3027
 Gly Ala Leu Gln Asn Gln Lys Asp Thr Val Leu Pro Arg Arg Ala Ile
 910 915 920

25 GAG AGG GAG GAG GGC CAG CTG CAG CTG TGT TCC CGT CAT AGG GAG AGC 3075
 Glu Arg Glu Glu Gly Gln Leu Gln Leu Cys Ser Arg His Arg Glu Ser
 925 930 935

30 TGAGACTCCC CGCCCGCCCT CCTCTGCCCC CTCCCCCGCA GACAGACAGA CAGACGGACG 3135
 GGACAGCGGC CCGGCCACG CAGAGCCCCG GAGCACCACG GGGTCGGGGG AGGAGCACCC 3195
 CCAGCCTCCC CCAGGCTGCG CCGCCCGCC CGCCGGTTGG CCGGCTGGCC GGTCCACCCC 3255

35 GTCCCGGCCC CGCGCGTGCC CCCAGCGTGG GGCTAACGGG CGCCTTGCT GTGTATTTCT 3315

	ATTTTGCAGC	AGIACCATCC	CACTGATATC	ACGGGCCCGC	TCAACCTCTC	AGATCCCTCG	3375
5	GTCAGCACCG	TGGTGTGAGG	CCCCCGGAGG	CGCCACACCTG	CCCAGTTAGC	CCGGCCAAGG	3435
	ACACTGATGG	GTCTTGCTGC	TCGGGAAGGC	CTGAGGGAAG	CCCACCCGCC	CCAGAGACTG	3495
	CCCACCCTGG	GCCTCCCGTC	CGTCCGCCCG	CCCACCCCGC	TGCCTGGCGG	GCAGCCCCTG	3555
10	CTGGACCAAG	GTGCGGACCG	GAGCGGCTGA	GGACGGGGCA	GAGCTGAGTC	GGCTGGGCAG	3615
	GGCCGCAGGG	CGCTCCGGCA	GAGGCAGGCC	CCTGGGGTCT	CTGAGCAGTG	GGGAGCGGGG	3675
	GCTAACTGCC	CCCAGGCGGA	GGGGCTTGGA	GCAGAGACGG	CAGCCCCATC	CTTCCCGCAG	3735
15	CACCAGCCTG	AGCCACAGTG	GGGCCCATGG	CCCCAGCTGG	CTGGGTGCGC	CCTCCTCGGG	3795
	CGCCTGCGCT	CCTCTGCAGC	CTGAGCTCCA	CCCTCCCCTC	TTCTTGCGGC	ACCGCCCACC	3855
20	AAACACCCCG	TCTGCCCTT	GACGCCACAC	GCCGGGGCTG	GCGCTGCCCT	CCCCCACGGC	3915
	CGTCCCTGAC	TTCCAGCTG	GCAGCGCCTC	CCGCCGCCTC	GGGCCGCCTC	CTCCAGAATC	3975
	GAGAGGGCTG	AGCCCCCTCT	CTCTCGTCC	GGCCTGCAGC	ACAGAAGGGG	GCCTCCCCGG	4035
25	GGGTCCCCGG	ACGCTGGCTC	GGGACTGTCT	TCAACCCTGC	CCTGCACCTT	GGGCACGGGA	4095
	GAGCGCCACC	CGCCCGCCCC	CGCCCTCGCT	CCGGGTGCGT	GACCGGCCCG	CCACCTTGTA	4155
30	CAGAACCAAGC	ACTCCCAGGG	CCCGAGCGCG	TGCCTTCCCC	GTGCGCAGCC	GCGCTCTGCC	4215
	CCTCCGTCCC	CAGGGTGCAG	GCGCGCACCG	CCCAACCCCC	ACCTCCCGGT	GTATGCAGTG	4275
	GTGATGCCCTA	AAGGAATGTC	ACG				4298
35							

(2) INFORMATION FOR SEQ ID NO:2:

(1) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 938 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	Met	Ser	Thr	Met	Arg	Leu	Leu	Thr	Leu	Ala	Leu	Leu	Phe	Ser	Cys	Ser
15	1				5					10					15	
	Val	Ala	Arg	Ala	Ala	Cys	Asp	Pro	Lys	Ile	Val	Asn	Ile	Gly	Ala	Val
				20					25					30		
20	Leu	Ser	Thr	Arg	Lys	His	Glu	Gln	Met	Phe	Arg	Glu	Ala	Val	Asn	Gln
			35					40					45			
	Ala	Asn	Lys	Arg	His	Gly	Ser	Trp	Lys	Ile	Gln	Leu	Asn	Ala	Thr	Ser
	50						55					60				
25	Val	Thr	His	Lys	Pro	Asn	Ala	Ile	Gln	Met	Ala	Leu	Ser	Val	Cys	Glu
	65					70					75					80
	Asp	Leu	Ile	Ser	Ser	Gln	Val	Tyr	Ala	Ile	Leu	Val	Ser	His	Pro	Pro
					85					90					95	
30	Thr	Pro	Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	Val	Ser	Tyr	Thr	Ala	Gly
				100					105					110		
	Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	Thr	Arg	Met	Ser	Ile	Tyr
35		115						120					125			

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	305					310										315												320
	Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr	Ala	Asp	Gly	Val	Thr	Gly												
					325						330																	335
5																												
	Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	Arg	Lys	Phe	Ala	Asn	Tyr	Ser												
					340						345					350												
10	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	Gln	Val	Gly	Ile	Tyr	Asn												
					355						360					365												
	Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	Ile	Ile	Trp	Pro	Gly	Gly												
					370					375					380													
15	Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met	Ser	Thr	Arg	Leu	Lys	Ile												
	Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr	Val	Lys	Pro	Thr	Leu	Ser												
					405						410					415												
20																												
	Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val	Asn	Gly	Asp	Pro	Val	Lys												
					420						425					430												
	Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr	Ser	Pro	Gly	Ser	Pro	Arg												
25					435						440					445												
	His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe	Cys	Ile	Asp	Leu	Leu	I												

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	Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met	
	500	505 510
5	Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu	
	515	520 525
	Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys	
	530	535 540
10	Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser	
	545	550 555 560
	Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val Met	
	565	570 575
15	Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn	
	580	585 590
	Ser Glu Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp	
20	595	600 605
	Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro	
	610	615 620
25	Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala	
	625	630 635 640
	Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val	
	645	650 655
30	Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu	
	660	665 670
	Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser	
35	675	680 685

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865 870 875 880

Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser

885 890 895

5

Ser Lys Asp Thr Ser Thr Gly Gly Gly Arg Gly Ala Leu Gln Asn Gln

900 905 910

Lys Asp Thr Val Leu Pro Arg Arg Ala Ile Glu Arg Glu Glu Gly Gln

10

915 920 925

Leu Gln Leu Cys Ser Arg His Arg Glu Ser

930 935

15

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 base pairs

20

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

25

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..63

30

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGT AAA AAA AGG AAC TAT GAA AAC CTC GAC CAA CTG TCC TAT GAC AAC 48

Ser Lys Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn

1 5 10 15

35

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AAG CGC GGA CCC AAG

63

Lys Arg Gly Pro Lys

20

5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

10

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser Lys Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn

1

5

10

15

20

Lys Arg Gly Pro Lys

20

(2) INFORMATION FOR SEQ ID NO:5:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4340 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

30

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

35

(A) NAME/KEY: CDS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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	Phe	Glu	Asp	Asn	Val	Asp	Thr	Glu	Ala	Val	Ala	Gln	Ile	Leu	Asp	Phe	
	95					100						105				110	
5	ATC	TCC	TCC	CAG	ACC	CAT	GTG	CCC	ATC	CTC	AGC	ATC	AGC	GGA	GGC	TCT	566
	Ile	Ser	Ser	Gln	Thr	His	Val	Pro	Ile	Leu	Ser	Ile	Ser	Gly	Gly	Ser	
					115					120					125		
	GCT	GTG	GTC	CTC	ACC	CCC	AAG	GAG	CCG	GGC	TCC	GCC	TTC	CTG	CAG	CTG	614
10	Ala	Val	Val	Leu	Thr	Pro	Lys	Glu	Pro	Gly	Ser	Ala	Phe	Leu	Gln	Leu	
				130						135					140		
	GGC	GTG	TCC	CTG	GAG	CAG	CAG	CTG	CAG	GTG	CTG	TTC	AAG	GTG	CTG	GAA	662
	Gly	Val	Ser	Leu	Glu	Gln	Gln	Leu	Gln	Val	Leu	Phe	Lys	Val	Leu	Glu	
				145					150					155			
15																	
	GAG	TAC	GAC	TGG	AGC	GCC	TTC	GCC	GTC	ATC	ACC	AGC	CTG	CAC	CCG	GGC	710
	Glu	Tyr	Asp	Trp	Ser	Ala	Phe	Ala	Val	Ile	Thr	Ser	Leu	His	Pro	Gly	
		160					165					170					
20	CAC	GCG	CTC	TTC	CTG	GAG	GGC	GTG	CGC	GCC	GTC	GCC	GAC	GCC	AGC	CAC	758
	His	Ala	Leu	Phe	Leu	Glu	Gly	Val	Arg	Ala	Val	Ala	Asp	Ala	Ser	His	
	175					180					185				190		
	GTG	AGT	TGG	CGG	CTG	CTG	GAC	GTG	GTC	ACG	CTG	GAA	CTG	GAC	CCG	GGA	806
25	Val	Ser	Trp	Arg	Leu	Leu	Asp	Val	Val	Thr	Leu	Glu	Leu	Asp	Pro	Gly	
				195						200				205			
	GGG	CCG	CGC	GCG	CGC	ACG	CAG	CGC	CTG	CTG	CGC	CAG	CTC	GAC	GCG	CCC	854
30	Gly	Pro	Arg	Ala	Arg	Thr	Gln	Arg	Leu	Leu	Arg	Gln	Leu	Asp	Ala	Pro	
				210						215				220			
	GTG	TTT	GTG	GCC	TAC	TGC	TCG	CGC	GAG	GAG	GCC	GAG	GTG	CTC	TTC	GCC	902
	Val	Phe	Val	Ala	Tyr	Cys	Ser	Arg	Glu	Glu	Ala	Glu	Val	Leu	Phe	Ala	
				225					230					235			
35																	

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	GAG GCG GCG CAG GCC GGT CTG GTG GGG CCC GGC CAC GTG TGG CTG GTG	950
	Glu Ala Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val	
	240 245 250	
5	CCC AAC CTG GCG CTG GGC AGC ACC GAT GCG CCC CCC GCC ACC TTC CCC	998
	Pro Asn Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro	
	255 260 265 270	
10	GTG GGC CTC ATC AGC GTC GTC ACC GAG AGC TGG CGC CTC AGC CTG CGC	1046
	Val Gly Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg	
	275 280 285	
15	CAG AAG GTG CGC GAC GGC GTG GCC ATT CTG GCC CTG GGC GCC CAC AGC	1094
	Gln Lys Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser	
	290 295 300	
20	TAC TGG CGC CAG CAT GGA ACC CTG CCA GCC CCG GCC GGG GAC TGC CGT	1142
	Tyr Trp Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg	
	305 310 315	
25	GTT CAC CCT GGG CCC GTC AGC CCT GCC CGG GAG GCC TTC TAC AGG CAC	1190
	Val His Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His	
	320 325 330	
30	CTA CTG AAT GTC ACC TGG GAG GGC CGA GAC TTC TCC TTC AGC CCT GGT	1238
	Leu Leu Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly	
	335 340 345 350	
35	GGG TAC CTG GTC CAG CCC ACC ATG GTG GTG ATC GCC CTC AAC CGG CAC	1286
	Gly Tyr Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His	
	355 360 365	
40	CGC CTC TGG GAG ATG GTG GGG CGC TGG GAG CAT GGC GTC CTA TAC ATG	1334
	Arg Leu Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met	
	370 375 380	

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	AAG TAC CCC GTG TGG CCT CGC TAC AGT GCC TCT CTG CAG CCT GTG GTG	1382
	Lys Tyr Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val	
	385 390 395	
5		
	GAC AGT CGG CAC CTG ACG GTG GCC ACG CTG GAA GAG CGG CCC TTT GTC	1430
	Asp Ser Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val	
	400 405 410	
10		
	ATC GTG GAG AGC CCT GAC CCT GGC ACA GGA GGC TGT GTC CCC AAC ACC	1478
	Ile Val Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr	
	415 420 425 430	
	GTG CCC TGC CGC AGG CAG AGC AAC CAC ACC TTC AGC AGC GGG GAC GTG	1526
15	Val Pro Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val	
	435 440 445	
	GCC CCC TAC ACC AAG CTC TGC TGT AAG GGA TTC TGC ATC GAC ATC CTC	1574
	Ala Pro Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu	
20	450 455 460	
	AAG AAG CTG GCC AGA GTG GTC AAA TTC TCC TAC GAC CTG TAC CTG GTG	1622
	Lys Lys Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val	
	465 470 475	
25		
	ACC AAC GGC AAG CAT GGC AAG CGG GTG CGC GGC GTA TGG AAC GGC ATG	1670
	Thr Asn Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met	
	480 485 490	
30		
	ATT GGG GAG GTG TAC TAC AAG CGG GCA GAC ATG GCC ATC GGC TCC CTC	1718
	Ile Gly Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu	
	495 500 505 510	
	ACC ATC AAT GAG GAA CGC TCC GAG ATC GTA GAC TTC TCT GTA CCC TTT	1766
35	Thr Ile Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe	

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	Gln	Tyr	Ile	Asp	Thr	Val	Ser	Gly	Leu	Ser	Asp	Lys	Lys	Phe	Gln	Arg	
	655						660					665				670	
5	CCT	CAA	GAT	CAG	TAC	CCA	CCT	TTC	CGC	TTC	GGC	ACG	GTG	CCC	AAC	GGC	2246
	Pro	Gln	Asp	Gln	Tyr	Pro	Pro	Phe	Arg	Phe	Gly	Thr	Val	Pro	Asn	Gly	
					675					680					685		
10	AGC	ACG	GAG	CGG	AAC	ATC	CGC	AGT	AAC	TAC	CGT	GAC	ATG	CAC	ACC	CAC	2294
	Ser	Thr	Glu	Arg	Asn	Ile	Arg	Ser	Asn	Tyr	Arg	Asp	Met	His	Thr	His	
					690					695				700			
15	ATG	GTC	AAG	TTC	AAC	CAG	CGC	TCG	GTG	GAG	GAC	GCG	CTC	ACC	AGC	CTC	2342
	Met	Val	Lys	Phe	Asn	Gln	Arg	Ser	Val	Glu	Asp	Ala	Leu	Thr	Ser	Leu	
			705						710				715				
20	AAG	ATG	GGG	AAG	CTG	GAT	GCC	TTC	ATC	TAT	GAT	GCT	GCT	GTC	CTC	AAC	2390
	Lys	Met	Gly	Lys	Leu	Asp	Ala	Phe	Ile	Tyr	Asp	Ala	Ala	Val	Leu	Asn	
			720					725					730				
25	TAC	ATG	GCA	GGC	AAG	GAC	GAG	GGC	TGC	AAG	CTG	GTC	ACC	ATT	GGG	TCT	2438
	Tyr	Met	Ala	Gly	Lys	Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	Ile	Gly	Ser	
	735					740					745				750		
30	GGC	AAG	GTC	TTT	GCT	ACC	ACT	GGC	TAC	GGC	ATC	GCC	ATG	CAG	AAG	GAC	2486
	Gly	Lys	Val	Phe	Ala	Thr	Thr	Gly	Tyr	Gly	Ile	Ala	Met	Gln	Lys	Asp	
					755					760				765			
35	TCC	CAC	TGG	AAG	CGG	GCC	ATA	GAC	CTG	GCG	CTC	TTG	CAG	TTC	CTG	GGG	2534
	Ser	His	Trp	Lys	Arg	Ala	Ile	Asp	Leu	Ala	Leu	Leu	Gln	Phe	Leu	Gly	
					770					775				780			
40	GAC	GGA	GAG	ACA	CAG	AAA	CTG	GAG	ACA	GTG	TGG	CTC	TCA	GGG	ATC	TGC	2582
	Asp	Gly	Glu	Thr	Gln	Lys	Leu	Glu	Thr	Val	Trp	Leu	Ser	Gly	Ile	Cys	
					785					790				795			

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	AGC CCA TGC CTG CCC ACC CCC GAC CCG CCC CCA GAG CCG AGC CCC ACG	3062
	Ser Pro Cys Leu Pro Thr Pro Asp Pro Pro Pro Glu Pro Ser Pro Thr	
	945 950 955	
5		
	GGC TGG GGA CCG CCA GAC GGG GGT CGC GCG GCG CTT GTG CGC AGG GCT	3110
	Gly Trp Gly Pro Pro Asp Gly Gly Arg Ala Ala Leu Val Arg Arg Ala	
	960 965 970	
10		
	CCG CAG CCC CCG GGC CGC CCC CCG ACG CCG GGG CCG CCC CTG TCC GAC	3158
	Pro Gln Pro Pro Gly Arg Pro Pro Thr Pro Gly Pro Pro Leu Ser Asp	
	975 980 985 990	
	GTC TCC CGA GTG TCG CGC CGC CCA GCC TGG GAG GCG CGG TGG CCG GTG	3206
15	Val Ser Arg Val Ser Arg Arg Pro Ala Trp Glu Ala Arg Trp Pro Val	
	995 1000 1005	
	CGG ACC GGG CAC TGC GGG AGG CAC CTC TCG GCC TCC GAG CGG CCC CTG	3254
	Arg Thr Gly His Cys Gly Arg His Leu Ser Ala Ser Glu Arg Pro Leu	
20	1010 1015 1020	
	TCG CCC GCG CGC TGT CAC TAC AGC TCC TTT CCT CGA GCC GAC CGA TCC	3302
	Ser Pro Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser	
	1025 1030 1035	
25		
	GGC CGC CCC TTC CTC CCG CTC TTC CCG GAG CCC CCG GAG CTG GAG GAC	3350
	Gly Arg Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp	
	1040 1045 1050	
30		
	CTG CCG CTG CTC GGT CCG GAG CAG CTG GCC CCG CGG GAG GCC CTG CTG	3398
	Leu Pro Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu	
	1055 1060 1065 1070	
	CAC GCG GCC TGG GCC CGG GGC TCG CGC CCG CGT CAC GCT TCC CTG CCC	3446
35	His Ala Ala Trp Ala Arg Gly Ser Arg Pro Arg His Ala Ser Leu Pro	

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	1075	1080	1085	
	AGC TCC GTG GCC GAG GCC TTC GCT CGG CCC AGC TCG CTG CCC GCT GGG			3494
	Ser Ser Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly			
5	1090	1095	1100	
	TGC ACC GGC CCC GCC TGC GCC CGC CCC GAC GGA CAC TCG GCC TGC AGG			3542
	Cys Thr Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg			
	1105	1110	1115	
10	CGC TTG GCG CAG GCG CAG TCG ATG TGC TTG CCG ATC TAC CGG GAG GCC			3590
	Arg Leu Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala			
	1120	1125	1130	
15	TGC CAG GAG GGC GAG CAG GCA GGG GCC CCC GCC TGG CAG CAC AGA CAG			3638
	Cys Gln Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln			
	1135	1140	1145	1150
	CAC GTC TGC CTG CAC GCC CAC GCC CAC CTG CCA TTT TGC TGG GGG GCT			3686
20	His Val Cys Leu His Ala His Ala His Leu Pro Phe Cys Trp Gly Ala			
	1155	1160	1165	
	GTC TGT CCT CAC CTT CCA CCC TGT GCC AGC CAC GGC TCC TGG CTC TCC			3734
	Val Cys Pro His Leu Pro Pro Cys Ala Ser His Gly Ser Trp Leu Ser			
25	1170	1175	1180	
	GGG GCC TGG GGG CCT CTG GGG CAC AGG GGC AGG ACT CTG GGG CTG GGC			3782
	Gly Ala Trp Gly Pro Leu Gly His Arg Gly Arg Thr Leu Gly Leu Gly			
	1185	1190	1195	
30	ACA GGC TAC AGA GAC AGT GGG GGA CTG GAC GAG ATC AGC AGG GTA GCC			3830
	Thr Gly Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Arg Val Ala			
	1200	1205	1210	
35	CGT GGG ACG CAA GGC TTC CCG GGA CCC TGC ACC TGG AGA CGG ATC TCC			3878

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Arg Gly Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser
 1215 1220 1225 1230

5 AGT CTG GAG TCA GAA GTG TGACTTATCA GCCACTCAGG CTCCGAGCCA 3926
 Ser Leu Glu Ser Glu Val
 1235

GCTGGATTCT CTGCCTGCCA CTGTCAGGGT TAAGCGGCAG GCAGGATTGG GCTTTTCTGG 3986

10 CTTCTACCAT GAAATCCTGG CCATGGGACC CCAGTGACAG ATGATGTCTT CCATGGTCAT 4046

CAGTGACCTC AGTAGCCTCA AATCATGGTG AGGGCTGGGC TTTTGCTGTC CTCTTCTCAC 4106

GCAGAGTTCT GCCAGGAGGG TGTGCTGTGG GGGTCAGACT CCTGAGGCTC TCCCTTCCCT 4166

15 GGGGCTAGCC AGTTACTGGT CATGCCTGCT GTGGGCATGG AGGCTGGAAC TTGTGGTTGA 4226

GGCAGGGCCA TCCCGATCCT TGCTCTACCT GGCTAGAGTT TCTTCTCATC AGAGCACTGG 4286

20 GACATTAAAC CCACCTTTTC CCAGAAAAAA AAAAAAAAAA AAAAAAAAAA AAAG 4340

(2) INFORMATION FOR SEQ ID NO:6:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1236 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu Phe Gly
 35 1 5 10 15

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	Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met Thr Val	
	20	25 30
5	Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe Arg Val	
	35	40 45
	Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile Gln Pro	
	50	55 60
10	Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu Thr Gln	
	65	70 75 80
	Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val Phe Glu	
15	85	90 95
	Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe Ile Ser	
	100	105 110
20	Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser Ala Val	
	115	120 125
	Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu Gly Val	
	130	135 140
25	Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu Glu Tyr	
	145	150 155 160
	Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly His Ala	
30	165	170 175
	Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His Val Ser	
	180	185 190
35	Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly Gly Pro	

195 200 205

Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro Val Phe
210 215 220

5 Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala Glu Ala
225 230 235 240

Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val Pro Asn
10 245 250 255

Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro Val Gly
260 265 270

15 Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg Gln Lys
275 280 285

Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser Tyr Trp
290 295 300

20 Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg Val His
305 310 315 320

Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His Leu Leu
25 325 330 335

Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly Gly Tyr
340 345 350

30 Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His Arg Leu
355 360 365

Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met Lys Tyr
370 375 380

35

Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val Asp Ser
385 390 395 400

Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val
5 405 410 415

Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr Val Pro
420 425 430

Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val Ala Pro
10 435 440 445

Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys
450 455 460

Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn
15 465 470 475 480

Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met Ile Gly
20 485 490 495

Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile
500 505 510

Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu
25 515 520 525

Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro
530 535 540

Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe
30 545 550 555 560

Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe Glu Tyr
35 565 570 575

	Phe	Ser	Pro	Val	Ser	Tyr	Asn	Gln	Asn	Leu	Thr	Arg	Gly	Lys	Lys	Ser
				580					585						590	
5	Gly	Gly	Pro	Ala	Phe	Thr	Ile	Gly	Lys	Ser	Val	Trp	Leu	Leu	Trp	Ala
			595					600					605			
	Leu	Val	Phe	Asn	Asn	Ser	Val	Pro	Ile	Glu	Asn	Pro	Arg	Gly	Thr	Thr
	610						615					620				
10	Ser	Lys	Ile	Met	Val	Leu	Val	Trp	Ala	Phe	Phe	Ala	Val	Ile	Phe	Leu
	625					630					635					640
	Ala	Arg	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Met	Ile	Gln	Glu	Gln	Tyr
15				645						650					655	
	Ile	Asp	Thr	Val	Ser	Gly	Leu	Ser	Asp	Lys	Lys	Phe	Gln	Arg	Pro	Gln
			660						665				670			
20	Asp	Gln	Tyr	Pro	Pro	Phe	Arg	Phe	Gly	Thr	Val	Pro	Asn	Gly	Ser	Thr
		675						680					685			
	Glu	Arg	Asn	Ile	Arg	Ser	Asn	Tyr	Arg	Asp	Met	His	Thr	His	Met	Val
	690						695					700				
25	Lys	Phe	Asn	Gln	Arg	Ser	Val	Glu	Asp	Ala	Leu	Thr	Ser	Leu	Lys	Met
	705					710					715					720
	Gly	Lys	Leu	Asp	Ala	Phe	Ile	Tyr	Asp	Ala	Ala	Val	Leu	Asn	Tyr	Met
30				725						730					735	
	Ala	Gly	Lys	Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	Ile	Gly	Ser	Gly	Lys
			740						745					750		
35	Val	Phe	Ala	Thr	Thr	Gly	Tyr	Gly	Ile	Ala	Met	Gln	Lys	Asp	Ser	His

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	755	760	765
	Trp Lys Arg Ala Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Gly		
	770	775	780
5	Glu Thr Gln Lys Leu Glu Thr Val Trp Leu Ser Gly Ile Cys Gln Asn		
	785	790	795 800
	Glu Lys Asn Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Ala		
10	805	810	815
	Gly Val Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ala Leu Leu Val		
	820	825	830
15	Phe Ala Trp Glu His Leu Val Tyr Trp Lys Leu Arg His Ser Val Pro		
	835	840	845
	Asn Ser Ser Gln Leu Asp Phe Leu Leu Ala Phe Ser Arg Gly Ile Tyr		
	850	855	860
20	Ser Cys Phe Ser Gly Val Gln Ser Leu Ala Ser Pro Pro Arg Gln Ala		
	865	870	875 880
	Ser Pro Asp Leu Thr Ala Ser Ser Ala Gln Ala Ser Val Leu Lys Met		
25	885	890	895
	Leu Gln Ala Ala Arg Asp Met Val Thr Thr Ala Gly Val Ser Ser Ser		
	900	905	910
30	Leu Asp Arg Ala Thr Arg Thr Ile Glu Asn Trp Gly Gly Gly Arg Arg		
	915	920	925
	Ala Pro Pro Pro Ser Pro Cys Pro Thr Pro Arg Ser Gly Pro Ser Pro		
	930	935	940
35			

Cys Leu Pro Thr Pro Asp Pro Pro Pro Glu Pro Ser Pro Thr Gly Trp
 945 950 955 960
 Gly Pro Pro Asp Gly Gly Arg Ala Ala Leu Val Arg Arg Ala Pro Gln
 5 965 970 975
 Pro Pro Gly Arg Pro Pro Thr Pro Gly Pro Pro Leu Ser Asp Val Ser
 980 985 990
 10 Arg Val Ser Arg Arg Pro Ala Trp Glu Ala Arg Trp Pro Val Arg Thr
 995 1000 1005
 Gly His Cys Gly Arg His Leu Ser Ala Ser Glu Arg Pro Leu Ser Pro
 1010 1015 1020
 15 Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg
 1025 1030 1035 1040
 Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro
 20 1045 1050 1055
 Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu His Ala
 1060 1065 1070
 25 Ala Trp Ala Arg Gly Ser Arg Pro Arg His Ala Ser Leu Pro Ser Ser
 1075 1080 1085
 Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr
 1090 1095 1100
 30 Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg Arg Leu
 1105 1110 1115 1120
 Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln
 35 1125 1130 1135

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Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln His Val
1140 1145 1150

5 Cys Leu His Ala His Ala His Leu Pro Phe Cys Trp Gly Ala Val Cys
1155 1160 1165

Pro His Leu Pro Pro Cys Ala Ser His Gly Ser Trp Leu Ser Gly Ala
1170 1175 1180

10 Trp Gly Pro Leu Gly His Arg Gly Arg Thr Leu Gly Leu Gly Thr Gly
1185 1190 1195 1200

Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Arg Val Ala Arg Gly
15 1205 1210 1215

Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu
1220 1225 1230

20 Glu Ser Glu Val
1235

(2) INFORMATION FOR SEQ ID NO:7:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

30

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

35

(A) NAME/KEY: CDS

(B) LOCATION: 2..22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

5 C TCT GAG GCT CAG CCT GTC CCC AG 24
Ser Glu Ala Gln Pro Val Pro
1 5

10 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

20

Ser Glu Ala Gln Pro Val Pro

1 5

25 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

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AGAAGGGGGT G

11

5 (2) INFORMATION FOR SEQ ID NO:10:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4808 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

15 (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 311..4705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

20

ATCATGGGAC CGGGTGAGCG CTGAGAATCG CGGCCGCAGC CATCAGCCCT GGAGATGACC 60

AGGAGCGGCC ACTGCTGAGA ACTATGTGGA GAGAGGCTGC GAGCCCTGCT GCAGAGCCTC 120

25 CGGCTGGGAT AGCCGCCCCC CGTGGGGGCG ATGCGGACAG CGCGGGACAG CCAGGGGAGC 180

GCGCTGGGGC CGCAGCATGC GGGAACCCGC TAAACCCGGT GGCTGCTGAG GCGGCCGAGA 240

TGCTCGTGCG CGCAGCGCGC CCCACTGCAT CCTCGACCTT CTCGGGCTAC AGGGACCGTC 300

30

AGTGGCGACT ATG GGC AGA GTG GGC TAT TGG ACC CTG CTG GTG CTG CCG 349

Met Gly Arg Val Gly Tyr Trp Thr Leu Leu Val Leu Pro

1 5 10

35 GCC CTT CTG GTC TGG CGC GGT CCG GCG CCG AGC GCG GCG GCG GAG AAG 397

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	Ala Leu Leu Val Trp Arg Gly Pro Ala Pro Ser Ala Ala Ala Glu Lys	
	15 20 25	
5	GGT CCC CCC GCG CTA AAT ATT GCG GTG ATG CTG GGT CAC AGC CAC GAC Gly Pro Pro Ala Leu Asn Ile Ala Val Met Leu Gly His Ser His Asp	445
	30 35 40 45	
10	GTG ACA GAG CGC GAA CTT CGA ACA CTG TGG GGC CCC GAG CAG GCG GCG Val Thr Glu Arg Glu Leu Arg Thr Leu Trp Gly Pro Glu Gln Ala Ala	493
	50 55 60	
15	GGG CTG CCC CTG GAC GTG AAC GTG GTA GCT CTG CTG ATG AAC CGC ACC Gly Leu Pro Leu Asp Val Asn Val Val Ala Leu Leu Met Asn Arg Thr	541
	65 70 75	
20	GAC CCC AAG AGC CTC ATC ACG CAC GTG TGC GAC CTC ATG TCC GGG GCA Asp Pro Lys Ser Leu Ile Thr His Val Cys Asp Leu Met Ser Gly Ala	589
	80 85 90	
25	CGC ATC CAC GGC CTC GTG TTT GGG GAC GAC ACG GAC CAG GAG GCC GTA Arg Ile His Gly Leu Val Phe Gly Asp Asp Thr Asp Gln Glu Ala Val	637
	95 100 105	
30	GCC CAG ATG CTG GAT TTT ATC TCC TCC CAC ACC TTC GTC CCC ATC TTG Ala Gln Met Leu Asp Phe Ile Ser Ser His Thr Phe Val Pro Ile Leu	685
	110 115 120 125	
35	GGC ATT CAT GGG GGC GCA TCT ATG ATC ATG GCT GAC AAG GAT CCG ACG Gly Ile His Gly Gly Ala Ser Met Ile Met Ala Asp Lys Asp Pro Thr	733
	130 135 140	
40	TCT ACC TTC TTC CAG TTT GGA GCG TCC ATC CAG CAG CAA GCC ACG GTC Ser Thr Phe Phe Gln Phe Gly Ala Ser Ile Gln Gln Gln Ala Thr Val	781
	145 150 155	

	ATG CTG AAG ATC ATG CAG GAT TAT GAC TGG CAT GTC TTC TCC CTG GTG	829
	Met Leu Lys Ile Met Gln Asp Tyr Asp Trp His Val Phe Ser Leu Val	
	160 165 170	
5	ACC ACT ATC TTC CCT GGC TAC AGG GAA TTC ATC AGC TTC GTC AAG ACC	877
	Thr Thr Ile Phe Pro Gly Tyr Arg Glu Phe Ile Ser Phe Val Lys Thr	
	175 180 185	
10	ACA GTG GAC AAC AGC TTT GTG GGC TGG GAC ATG CAG AAT CTG ATC ACA	925
	Thr Val Asp Asn Ser Phe Val Gly Trp Asp Met Gln Asn Val Ile Thr	
	190 195 200 205	
15	CTG GAC ACT TCC TTT GAG GAT GCA AAG ACA CAA GTC CAG CTG AAG AAG	973
	Leu Asp Thr Ser Phe Glu Asp Ala Lys Thr Gln Val Gln Leu Lys Lys	
	210 215 220	
20	ATC CAC TCT TCT GTC ATC TTG CTC TAC TGT TCC AAA GAC GAG GCT GTT	1021
	Ile His Ser Ser Val Ile Leu Leu Tyr Cys Ser Lys Asp Glu Ala Val	
	225 230 235	
25	CTC ATT CTG AGT GAG GCC CGC TCC CTT GGC CTC ACC GGG TAT GAT TTC	1069
	Leu Ile Leu Ser Glu Ala Arg Ser Leu Gly Leu Thr Gly Tyr Asp Phe	
	240 245 250	
30	TTC TGG ATT GTC CCC AGC TTG GTC TCT GGG AAC ACG GAG CTC ATC CCA	1117
	Phe Trp Ile Val Pro Ser Leu Val Ser Gly Asn Thr Glu Leu Ile Pro	
	255 260 265	
35	AAA GAG TTT CCA TCG GGA CTC ATT TCT GTC TCC TAC GAT GAC TGG GAC	1165
	Lys Glu Phe Pro Ser Gly Leu Ile Ser Val Ser Tyr Asp Asp Trp Asp	
	270 275 280 285	
40	TAC AGC CTG GAG GCG AGA GTG AGG GAC GGC ATT GGC ATC CTA ACC ACC	1213
	Tyr Ser Leu Glu Ala Arg Val Arg Asp Gly Ile Gly Ile Leu Thr Thr	
	290 295 300	

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	GCT GCA TCT TCT ATG CTG GAG AAG TTC TCC TAC ATC CCC GAG GCC AAG	1261
	Ala Ala Ser Ser Met Leu Glu Lys Phe Ser Tyr Ile Pro Glu Ala Lys	
	305 310 315	
5		
	GCC AGC TGC TAC GGG CAG ATG GAG AGG CCA GAG GTC CCG ATG CAC ACC	1309
	Ala Ser Cys Tyr Gly Gln Met Glu Arg Pro Glu Val Pro Met His Thr	
	320 325 330	
10		
	TTG CAC CCA TTT ATG GTC AAT GTT ACA TGG GAT GGC AAA GAC TTA TCC	1357
	Leu His Pro Phe Met Val Asn Val Thr Trp Asp Gly Lys Asp Leu Ser	
	335 340 345	
	TTC ACT GAG GAA GGC TAC CAG GTG CAC CCC AGG CTG GTG GTG ATT GTG	1405
15	Phe Thr Glu Glu Gly Tyr Gln Val His Pro Arg Leu Val Val Ile Val	
	350 355 360 365	
	CTG AAC AAA GAC CGG GAA TGG GAA AAG GTG GGC AAG TGG GAG AAC CAT	1453
	Leu Asn Lys Asp Arg Glu Trp Glu Lys Val Gly Lys Trp Glu Asn His	
20	370 375 380	
	ACG CTG AGC CTG AGG CAC GCC GTG TGG CCC AGG TAC AAG TCC TTC TCC	1501
	Thr Leu Ser Leu Arg His Ala Val Trp Pro Arg Tyr Lys Ser Phe Ser	
	385 390 395	
25		
	GAC TGT GAG CCG GAT GAC AAC CAT CTC AGC ATC GTC ACC CTG GAG GAG	1549
	Asp Cys Glu Pro Asp Asp Asn His Leu Ser Ile Val Thr Leu Glu Glu	
	400 405 410	
30		
	GCC CCA TTC GTC ATC GTG GAA GAC ATA GAC CCC CTG ACC GAG ACG TGT	1597
	Ala Pro Phe Val Ile Val Glu Asp Ile Asp Pro Leu Thr Glu Thr Cys	
	415 420 425	
	GTG AGG AAC ACC GTG CCA TGT CGG AAG TTC GTC AAA ATC AAC AAT TCA	1645
35	Val Arg Asn Thr Val Pro Cys Arg Lys Phe Val Lys Ile Asn Asn Ser	

	430	435	440	445	
	ACC AAT GAG GGG ATG AAT GTG AAG AAA TGC TGC AAG GGG TTC TGC ATT				1693
	Thr Asn Glu Gly Met Asn Val Lys Lys Cys Cys Lys Gly Phe Cys Ile				
5		450	455	460	
	GAT ATT CTG AAG AAG CTT TCC AGA ACT GTG AAG TTT ACT TAC GAC CTC				1741
	Asp Ile Leu Lys Lys Leu Ser Arg Thr Val Lys Phe Thr Tyr Asp Leu				
	465	470	475		
10	TAT CTG GTG ACC AAT GGG AAG CAT GGC AAG AAA GTT AAC AAT GTG TGG				1789
	Tyr Leu Val Thr Asn Gly Lys His Gly Lys Lys Val Asn Asn Val Trp				
	480	485	490		
15	AAT GGA ATG ATC GGT GAA GTG GTC TAT CAA CGG GCA GTC ATG GCA GTT				1837
	Asn Gly Met Ile Gly Glu Val Val Tyr Gln Arg Ala Val Met Ala Val				
	495	500	505		
	GGC TCG CTC ACC ATC AAT GAG GAA CGT TCT GAA GTG GTG GAC TTC TCT				1885
20	Gly Ser Leu Thr Ile Asn Glu Glu Arg Ser Glu Val Val Asp Phe Ser				
	510	515	520	525	
	GTG CCC TTT GTG GAA ACG GGA ATC AGT GTC ATG GTT TCA AGA AGT AAT				1933
	Val Pro Phe Val Glu Thr Gly Ile Ser Val Met Val Ser Arg Ser Asn				
25	530	535	540		
	GGC ACC GTC TCA CCT TCT GCT TTT CTA GAA CCA TTC AGC GCC TCT GTC				1981
	Gly Thr Val Ser Pro Ser Ala Phe Leu Glu Pro Phe Ser Ala Ser Val				
	545	550	555		
30	TGG GTG ATG ATG TTT GTG ATG CTG CTC ATT GTT TCT GCC ATA GCT GTT				2029
	Trp Val Met Met Phe Val Met Leu Leu Ile Val Ser Ala Ile Ala Val				
	560	565	570		
35	TGG GTC TTG GAT TAC TCC AGC CCT GTT GGA TAC AAC AGA AAC TTA GCC				2077

[illegible]

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	GTC AGC CTG AAA ACG GGG AAG CTG GAC GCT TTC ATC TAC GAT GCC GCA	2509
	Val Ser Leu Lys Thr Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala	
	720 725 730	
5	GTC TTG AAT TAC AAG GCT GGG AGG GAT GAA GGC TGC AAG CTG GTG ACC	2557
	Val Leu Asn Tyr Lys Ala Gly Arg Asp Glu Gly Cys Lys Leu Val Thr	
	735 740 745	
10	ATC GGG AGT GGG TAC ATC TTT GCC ACC ACC GGT TAT GGA ATT GCC CTT	2605
	Ile Gly Ser Gly Tyr Ile Phe Ala Thr Thr Gly Tyr Gly Ile Ala Leu	
	750 755 760 765	
15	CAG AAA GGC TCT CCT TGG AAG AGG CAG ATC GAC CTG GCC TTG CTT CAG	2653
	Gln Lys Gly Ser Pro Trp Lys Arg Gln Ile Asp Leu Ala Leu Leu Gln	
	770 775 780	
20	TTT GTG GGT GAT GGT GAG ATG GAG GAG CTG GAG ACC CTG TGG CTC ACT	2701
	Phe Val Gly Asp Gly Glu Met Glu Glu Leu Glu Thr Leu Trp Leu Thr	
	785 790 795	
25	GGG ATC TGC CAC AAC GAG AAG AAC GAG GTG ATG AGC AGC CAG CTG GAC	2749
	Gly Ile Cys His Asn Glu Lys Asn Glu Val Met Ser Ser Gln Leu Asp	
	800 805 810	
30	ATT GAC AAC ATG GCG GGC GTA TTC TAC ATG CTG GCT GCC GCC ATG GCC	2797
	Ile Asp Asn Met Ala Gly Val Phe Tyr Met Leu Ala Ala Ala Met Ala	
	815 820 825	
35	CTT AGC CTC ATC ACC TTC ATC TGG GAG CAC CTC TTC TAC TGG AAG CTG	2845
	Leu Ser Leu Ile Thr Phe Ile Trp Glu His Leu Phe Tyr Trp Lys Leu	
	830 835 840 845	
	CGC TTC TGT TTC ACG GGC GTG TGC TCC GAC CGG CCT GGG TTG CTC TTC	2893
	Arg Phe Cys Phe Thr Gly Val Cys Ser Asp Arg Pro Gly Leu Leu Phe	
	850 855 860	

TCC ATC AGC AGG GGC ATC TAC AGC TGC ATT CAT GGA GTG CAC ATT GAA 2941
 Ser Ile Ser Arg Gly Ile Tyr Ser Cys Ile His Gly Val His Ile Glu
 865 870 875
 5
 GAA AAG AAG AAG TCT CCA GAC TTC AAT CTG ACG GGA TCC CAG AGC AAC 2989
 Glu Lys Lys Lys Ser Pro Asp Phe Asn Leu Thr Gly Ser Gln Ser Asn
 880 885 890
 10
 ATG TTA AAA CTC CTC CGG TCA GCC AAA AAC ATT TCC AGC ATG TCC AAC 3037
 Met Leu Lys Leu Leu Arg Ser Ala Lys Asn Ile Ser Ser Met Ser Asn
 895 900 905
 15
 ATG AAC TCC TCA AGA ATG GAC TCA CCC AAA AGA GCT GCT GAC TTC ATC 3085
 Met Asn Ser Ser Arg Met Asp Ser Pro Lys Arg Ala Ala Asp Phe Ile
 910 915 920 925
 20
 CAA AGA GGT TCC CTC ATC ATG GAC ATG GTT TCA GAT AAG GGG AAT TTG 3133
 Gln Arg Gly Ser Leu Ile Met Asp Met Val Ser Asp Lys Gly Asn Leu
 930 935 940
 25
 ATG TAC TCA GAC AAC AGG TCC TTT CAG GGG AAA GAG AGC ATT TTT GGA 3181
 Met Tyr Ser Asp Asn Arg Ser Phe Gln Gly Lys Glu Ser Ile Phe Gly
 945 950 955
 30
 GAC AAC ATG AAC GAA CTC CAA ACA TTT GTG GCC AAC CGG CAG AAG GAT 3229
 Asp Asn Met Asn Glu Leu Gln Thr Phe Val Ala Asn Arg Gln Lys Asp
 960 965 970
 35
 AAC CTC AAT AAC TAT GTA TTC CAG GGA CAA CAT CCT CTT ACT CTC AAT 3277
 Asn Leu Asn Asn Tyr Val Phe Gln Gly Gln His Pro Leu Thr Leu Asn
 975 980 985
 35
 GAG TCC AAC CCT AAC ACG GTG GAG GTG GCC GTG AGC ACA GAA TCC AAA 3325
 Glu Ser Asn Pro Asn Thr Val Glu Val Ala Val Ser Thr Glu Ser Lys

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	990	995	1000	1005	
	GCG AAC TCT AGA CCC CGG CAG CTG TGG AAG AAA TCC GTG GAT TCC ATA				3373
	Ala Asn Ser Arg Pro Arg Gln Leu Trp Lys Lys Ser Val Asp Ser Ile				
5		1010	1015	1020	
	CGC CAG GAT TCA CTA TCC CAG AAT CCA GTC TCC CAG AGG GAT GAG GCA				3421
	Arg Gln Asp Ser Leu Ser Gln Asn Pro Val Ser Gln Arg Asp Glu Ala				
		1025	1030	1035	
10					
	ACA GCA GAG AAT AGG ACC CAC TCC CTA AAG AGC CCT AGG TAT CTT CCA				3469
	Thr Ala Glu Asn Arg Thr His Ser Leu Lys Ser Pro Arg Tyr Leu Pro				
		1040	1045	1050	
15					
	GAA GAG ATG GCC CAC TCT GAC ATT TCA GAA ACG TCA AAT CGG GCC ACG				3517
	Glu Glu Met Ala His Ser Asp Ile Ser Glu Thr Ser Asn Arg Ala Thr				
		1055	1060	1065	
	TGC CAC AGG GAA CCT GAC AAC AGT AAG AAC CAC AAA ACC AAG GAC AAC				3565
20	Cys His Arg Glu Pro Asp Asn Ser Lys Asn His Lys Thr Lys Asp Asn				
		1070	1075	1080	1085
	TTT AAA AGG TCA GTG GCC TCC AAA TAC CCC AAG GAC TGT AGT GAG GTC				3613
	Phe Lys Arg Ser Val Ala Ser Lys Tyr Pro Lys Asp Cys Ser Glu Val				
25		1090	1095	1100	
	GAG CGC ACC TAC CTG AAA ACC AAA TCA AGC TCC CCT AGA GAC AAG ATC				3661
	Glu Arg Thr Tyr Leu Lys Thr Lys Ser Ser Ser Pro Arg Asp Lys Ile				
		1105	1110	1115	
30					
	TAC ACT ATA GAT GGT GAG AAG GAG CCT GGT TTC CAC TTA GAT CCA CCC				3709
	Tyr Thr Ile Asp Gly Glu Lys Glu Pro Gly Phe His Leu Asp Pro Pro				
		1120	1125	1130	
35					
	CAG TTT GTT GAA AAT GTG ACC CTG CCC GAG AAC GTG GAC TTC CCG GAC				3757

Gln Phe Val Glu Asn Val Thr Leu Pro Glu Asn Val Asp Phe Pro Asp
1135 1140 1145

CCC TAC CAG GAT CCC AGT GAA AAC TTC CGC AAG GGG GAC TCC ACG CTG 3805
5 Pro Tyr Gln Asp Pro Ser Glu Asn Phe Arg Lys Gly Asp Ser Thr Leu
1150 1155 1160 1165

CCA ATG AAC CGG AAC CCC TTG CAT AAT GAA GAG GGG CTT TCC AAC AAC 3853
10 Pro Met Asn Arg Asn Pro Leu His Asn Glu Glu Gly Leu Ser Asn Asn
1170 1175 1180

GAC CAG TAT AAA CTC TAC TCC AAG CAC TTC ACC TTG AAA GAC AAG GGT 3901
Asp Gln Tyr Lys Leu Tyr Ser Lys His Phe Thr Leu Lys Asp Lys Gly
1185 1190 1195

15 TCC CCG CAC AGT GAG ACC AGC GAG CGA TAC CGG CAG AAC TCC ACG CAC 3949
Ser Pro His Ser Glu Thr Ser Glu Arg Tyr Arg Gln Asn Ser Thr His
1200 1205 1210

20 TGC AGA AGC TGC CTT TCC AAC ATG CCC ACC TAT TCA GGC CAC TTC ACC 3997
Cys Arg Ser Cys Leu Ser Asn Met Pro Thr Tyr Ser Gly His Phe Thr
1215 1220 1225

ATG AGG TCC CCC TTC AAG TGC GAT GCC TGC CTG CGG ATG GGG AAC CTC 4045
25 Met Arg Ser Pro Phe Lys Cys Asp Ala Cys Leu Arg Met Gly Asn Leu
1230 1235 1240 1245

TAT GAC ATC GAT GAA GAC CAG ATG CTT CAG GAG ACA GGT AAC CCA GCC 4093
Tyr Asp Ile Asp Glu Asp Gln Met Leu Gln Glu Thr Gly Asn Pro Ala
30 1250 1255 1260

ACC GGG GAG CAG GTC TAC CAG CAG GAC TGG GCA CAG AAC AAT GCC CTT 4141
Thr Gly Glu Gln Val Tyr Gln Gln Asp Trp Ala Gln Asn Asn Ala Leu
1265 1270 1275

35

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	CAA TTA CAA AAG AAC AAG CTA AGG ATT AGC CGT CAG CAT TCC TAC GAT	4189
	Gln Leu Gln Lys Asn Lys Leu Arg Ile Ser Arg Gln His Ser Tyr Asp	
	1280 1285 1290	
5	AAC ATT GTC GAC AAA CCT AGG GAG CTA GAC CTT AGC AGG CCC TCC CGG	4237
	Asn Ile Val Asp Lys Pro Arg Glu Leu Asp Leu Ser Arg Pro Ser Arg	
	1295 1300 1305	
10	AGC ATA AGC CTC AAG GAC AGG GAA CGG CTT CTG GAG GGA AAT TTT TAC	4285
	Ser Ile Ser Leu Lys Asp Arg Glu Arg Leu Leu Glu Gly Asn Phe Tyr	
	1310 1315 1320 1325	
15	GGC AGC CTG TTT AGT GTC CCC TCA AGC AAA CTC TCG GGG AAA AAA AGC	4333
	Gly Ser Leu Phe Ser Val Pro Ser Ser Lys Leu Ser Gly Lys Lys Ser	
	1330 1335 1340	
20	TCC CTT TTC CCC CAA GGT CTG GAG GAC AGC AAG AGG AGC AAG TCT CTC	4381
	Ser Leu Phe Pro Gln Gly Leu Glu Asp Ser Lys Arg Ser Lys Ser Leu	
	1345 1350 1355	
25	TTG CCA GAC CAC ACC TCC GAT AAC CCT TTC CTC CAC TCC CAC AGG GAT	4429
	Leu Pro Asp His Thr Ser Asp Asn Pro Phe Leu His Ser His Arg Asp	
	1360 1365 1370	
30	GAC CAA CGC TTG GTT ATT GGG AGA TGC CCC TCG GAC CCT TAC AAA CAC	4477
	Asp Gln Arg Leu Val Ile Gly Arg Cys Pro Ser Asp Pro Tyr Lys His	
	1375 1380 1385	
35	TCG TTG CCA TCC CAG GCG GTG AAT GAC AGC TAT CTT CGG TCG TCC TTG	4525
	Ser Leu Pro Ser Gln Ala Val Asn Asp Ser Tyr Leu Arg Ser Ser Leu	
	1390 1395 1400 1405	
	AGG TCA ACG GCA TCG TAC TGT TCC AGG GAC AGT CGG GGC CAC AAT GAT	4573
	Arg Ser Thr Ala Ser Tyr Cys Ser Arg Asp Ser Arg Gly His Asn Asp	
	1410 1415 1420	

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GTG TAT ATT TCG GAG CAT GTT ATG CCT TAT GCT GCA AAT AAG AAT AAT 4621
Val Tyr Ile Ser Glu His Val Met Pro Tyr Ala Ala Asn Lys Asn Asn
1425 1430 1435

5

ATG TAC TCT ACC CCC AGG GTT TTA AAT TCC TGC AGC AAT AGA CGC GTG 4669
Met Tyr Ser Thr Pro Arg Val Leu Asn Ser Cys Ser Asn Arg Arg Val
1440 1445 1450

10

TAC AAG GAA ATG CCT AGT ATC GAA TCT GAT GTT TAAAAATCTT CCAITTAATGT 4722
Tyr Lys Glu Met Pro Ser Ile Glu Ser Asp Val
1455 1460 1465

15

TTTATCTATA GGGAAATACA CGTAATGGCC AATGTTCTGG AGGGTAAATG TTGGATGTCC 4782

AATAGTGCCC TGCTAAGAGG AAGGAG 4808

(2) INFORMATION FOR SEQ ID NO:11:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1464 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: protein

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:11:

30

Met Gly Arg Val Gly Tyr Trp Thr Leu Leu Val Leu Pro Ala Leu Leu
1 5 10 15

Val Trp Arg Gly Pro Ala Pro Ser Ala Ala Ala Glu Lys Gly Pro Pro
20 25 30

35

	Ala	Leu	Asn	Ile	Ala	Val	Met	Leu	Gly	His	Ser	His	Asp	Val	Thr	Glu
	35						40						45			
5	Arg	Glu	Leu	Arg	Thr	Leu	Trp	Gly	Pro	Glu	Gln	Ala	Ala	Gly	Leu	Pro
	50						55						60			
	Leu	Asp	Val	Asn	Val	Val	Ala	Leu	Leu	Met	Asn	Arg	Thr	Asp	Pro	Lys
	65			70						75						80
10	Ser	Leu	Ile	Thr	His	Val	Cys	Asp	Leu	Met	Ser	Gly	Ala	Arg	Ile	His
				85						90						95
	Gly	Leu	Val	Phe	Gly	Asp	Asp	Thr	Asp	Gln	Glu	Ala	Val	Ala	Gln	Met
	100						105						110			
15	Leu	Asp	Phe	Ile	Ser	Ser	His	Thr	Phe	Val	Pro	Ile	Leu	Gly	Ile	His
	115						120						125			
	Gly	Gly	Ala	Ser	Met	Ile	Met	Ala	Asp	Lys	Asp	Pro	Thr	Ser	Thr	Phe
20	130						135						140			
	Phe	Gln	Phe	Gly	Ala	Ser	Ile	Gln	Gln	Gln	Ala	Thr	Val	Met	Leu	Lys
	145			150						155						160
25	Ile	Met	Gln	Asp	Tyr	Asp	Trp	His	Val	Phe	Ser	Leu	Val	Thr	Thr	Ile
				165						170						175
	Phe	Pro	Gly	Tyr	Arg	Glu	Phe	Ile	Ser	Phe	Val	Lys	Thr	Thr	Val	Asp
	180						185						190			
30	Asn	Ser	Phe	Val	Gly	Trp	Asp	Met	Gln	Asn	Val	Ile	Thr	Leu	Asp	Thr
	195						200						205			
	Ser	Phe	Glu	Asp	Ala	Lys	Thr	Gln	Val	Gln	Leu	Lys	Lys	Ile	His	Ser
35	210						215						220			

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Ser Val Ile Leu Leu Tyr Cys Ser Lys Asp Glu Ala Val Leu Ile Leu
225 230 235 240

5 Ser Glu Ala Arg Ser Leu Gly Leu Thr Gly Tyr Asp Phe Phe Trp Ile
245 250 255

Val Pro Ser Leu Val Ser Gly Asn Thr Glu Leu Ile Pro Lys Glu Phe
260 265 270

10 Pro Ser Gly Leu Ile Ser Val Ser Tyr Asp Asp Trp Asp Tyr Ser Leu
275 280 285

Glu Ala Arg Val Arg Asp Gly Ile Gly Ile Leu Thr Thr Ala Ala Ser
15 290 295 300

Ser Met Leu Glu Lys Phe Ser Tyr Ile Pro Glu Ala Lys Ala Ser Cys
305 310 315 320

20 Tyr Gly Gln Met Glu Arg Pro Glu Val Pro Met His Thr Leu His Pro
325 330 335

Phe Met Val Asn Val Thr Trp Asp Gly Lys Asp Leu Ser Phe Thr Glu
340 345 350

25 Glu Gly Tyr Gln Val His Pro Arg Leu Val Val Ile Val Leu Asn Lys
355 360 365

Asp Arg Glu Trp Glu Lys Val Gly Lys Trp Glu Asn His Thr Leu Ser
30 370 375 380

Leu Arg His Ala Val Trp Pro Arg Tyr Lys Ser Phe Ser Asp Cys Glu
385 390 395 400

35 Pro Asp Asp Asn His Leu Ser Ile Val Thr Leu Glu Glu Ala Pro Phe

[illegible]

Ala Pro His Gly Pro Ser Phe Thr Ile Gly Lys Ala Ile Trp Leu Leu
595 600 605

Trp Gly Leu Val Phe Asn Asn Ser Val Pro Val Gln Asn Pro Lys Gly
5 610 615 620

Thr Thr Ser Lys Ile Met Val Ser Val Trp Ala Phe Phe Ala Val Ile
625 630 635 640

10 Phe Leu Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu
645 650 655

Glu Phe Val Asp Gln Val Thr Gly Leu Ser Asp Lys Lys Phe Gln Arg
660 665 670

15 Pro His Asp Tyr Ser Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly
675 680 685

Ser Thr Glu Arg Asn Ile Arg Asn Asn Tyr Pro Tyr Met His Gln Tyr
20 690 695 700

Met Thr Lys Phe Asn Gln Lys Gly Val Glu Asp Ala Leu Val Ser Leu
705 710 715 720

25 Lys Thr Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn
725 730 735

Tyr Lys Ala Gly Arg Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser
740 745 750

30 Gly Tyr Ile Phe Ala Thr Thr Gly Tyr Gly Ile Ala Leu Gln Lys Gly
755 760 765

Ser Pro Trp Lys Arg Gln Ile Asp Leu Ala Leu Leu Gln Phe Val Gly
35 770 775 780

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	Asp Gly Glu Met Glu Glu Leu Glu Thr Leu Trp Leu Thr Gly Ile Cys	
	785	790 795 800
5	His Asn Glu Lys Asn Glu Val Met Ser Ser Gln Leu Asp Ile Asp Asn	
		805 810 815
	Met Ala Gly Val Phe Tyr Met Leu Ala Ala Ala Met Ala Leu Ser Leu	
		820 825 830
10	Ile Thr Phe Ile Trp Glu His Leu Phe Tyr Trp Lys Leu Arg Phe Cys	
		835 840 845
	Phe Thr Gly Val Cys Ser Asp Arg Pro Gly Leu Leu Phe Ser Ile Ser	
15		850 855 860
	Arg Gly Ile Tyr Ser Cys Ile His Gly Val His Ile Glu Glu Lys Lys	
		865 870 875 880
20	Lys Ser Pro Asp Phe Asn Leu Thr Gly Ser Gln Ser Asn Met Leu Lys	
		885 890 895
	Leu Leu Arg Ser Ala Lys Asn Ile Ser Ser Met Ser Asn Met Asn Ser	
		900 905 910
25	Ser Arg Met Asp Ser Pro Lys Arg Ala Ala Asp Phe Ile Gln Arg Gly	
		915 920 925
	Ser Leu Ile Met Asp Met Val Ser Asp Lys Gly Asn Leu Met Tyr Ser	
30		930 935 940
	Asp Asn Arg Ser Phe Gln Gly Lys Glu Ser Ile Phe Gly Asp Asn Met	
		945 950 955 960
35	Asn Glu Leu Gln Thr Phe Val Ala Asn Arg Gln Lys Asp Asn Leu Asn	

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	965	970	975
	Asn Tyr Val Phe Gln Gly Gln His Pro Leu Thr Leu Asn Glu Ser Asn		
	980	985	990
5	Pro Asn Thr Val Glu Val Ala Val Ser Thr Glu Ser Lys Ala Asn Ser		
	995	1000	1005
	Arg Pro Arg Gln Leu Trp Lys Lys Ser Val Asp Ser Ile Arg Gln Asp		
10	1010	1015	1020
	Ser Leu Ser Gln Asn Pro Val Ser Gln Arg Asp Glu Ala Thr Ala Glu		
	1025	1030	1035
	1040		
15	Asn Arg Thr His Ser Leu Lys Ser Pro Arg Tyr Leu Pro Glu Glu Met		
	1045	1050	1055
	Ala His Ser Asp Ile Ser Glu Thr Ser Asn Arg Ala Thr Cys His Arg		
	1060	1065	1070
20	Glu Pro Asp Asn Ser Lys Asn His Lys Thr Lys Asp Asn Phe Lys Arg		
	1075	1080	1085
	Ser Val Ala Ser Lys Tyr Pro Lys Asp Cys Ser Glu Val Glu Arg Thr		
25	1090	1095	1100
	Tyr Leu Lys Thr Lys Ser Ser Ser Pro Arg Asp Lys Ile Tyr Thr Ile		
	1105	1110	1115
	1120		
30	Asp Gly Glu Lys Glu Pro Gly Phe His Leu Asp Pro Pro Gln Phe Val		
	1125	1130	1135
	Glu Asn Val Thr Leu Pro Glu Asn Val Asp Phe Pro Asp Pro Tyr Gln		
	1140	1145	1150
35			

Asp Pro Ser Glu Asn Phe Arg Lys Gly Asp Ser Thr Leu Pro Met Asn
1155 1160 1165

Arg Asn Pro Leu His Asn Glu Glu Gly Leu Ser Asn Asn Asp Gln Tyr
5 1170 1175 1180

Lys Leu Tyr Ser Lys His Phe Thr Leu Lys Asp Lys Gly Ser Pro His
1185 1190 1195 1200

Ser Glu Thr Ser Glu Arg Tyr Arg Gln Asn Ser Thr His Cys Arg Ser
10 1205 1210 1215

Cys Leu Ser Asn Met Pro Thr Tyr Ser Gly His Phe Thr Met Arg Ser
1220 1225 1230

Pro Phe Lys Cys Asp Ala Cys Leu Arg Met Gly Asn Leu Tyr Asp Ile
15 1235 1240 1245

Asp Glu Asp Gln Met Leu Gln Glu Thr Gly Asn Pro Ala Thr Gly Glu
20 1250 1255 1260

Gln Val Tyr Gln Gln Asp Trp Ala Gln Asn Asn Ala Leu Gln Leu Gln
1265 1270 1275 1280

Lys Asn Lys Leu Arg Ile Ser Arg Gln His Ser Tyr Asp Asn Ile Val
25 1285 1290 1295

Asp Lys Pro Arg Glu Leu Asp Leu Ser Arg Pro Ser Arg Ser Ile Ser
1300 1305 1310

Leu Lys Asp Arg Glu Arg Leu Leu Glu Gly Asn Phe Tyr Gly Ser Leu
30 1315 1320 1325

Phe Ser Val Pro Ser Ser Lys Leu Ser Gly Lys Lys Ser Ser Leu Phe
35 1330 1335 1340

Pro Gln Gly Leu Glu Asp Ser Lys Arg Ser Lys Ser Leu Leu Pro Asp
1345 1350 1355 1360

5 His Thr Ser Asp Asn Pro Phe Leu His Ser His Arg Asp Asp Gln Arg
1365 1370 1375

Leu Val Ile Gly Arg Cys Pro Ser Asp Pro Tyr Lys His Ser Leu Pro
1380 1385 1390

10 Ser Gln Ala Val Asn Asp Ser Tyr Leu Arg Ser Ser Leu Arg Ser Thr
1395 1400 1405

Ala Ser Tyr Cys Ser Arg Asp Ser Arg Gly His Asn Asp Val Tyr Ile
15 1410 1415 1420

Ser Glu His Val Met Pro Tyr Ala Ala Asn Lys Asn Asn Met Tyr Ser
1425 1430 1435 1440

20 Thr Pro Arg Val Leu Asn Ser Cys Ser Asn Arg Arg Val Tyr Lys Glu
1445 1450 1455

Met Pro Ser Ile Glu Ser Asp Val
1460

25

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

35 (ii) MOLECULE TYPE: cDNA

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(x1) SEQUENCE DESCRIPTION: SEQ ID NO:12:

5 CGAGGGAGGC GGCCGGCGCG GACTCTCTTC GCGGGCGCAG CGCCCCTTCC CCTTCGGACC 60
CTCCGGTGGA CATG 74

(2) INFORMATION FOR SEQ ID NO:13:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

15

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

20

- (A) NAME/KEY: CDS
- (B) LOCATION: 210..4664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

25 TTGAATTTGC ATCTCTTCAA GACACAAGAT TAAAACAAAA TTTACGCTAA ATTGGATTTT 60
AAATTATCTT CCGTTCATTT ATCCTTCGTC TTCTTATGT GGATATGCAA GCGAGAAGAA 120
GGGACTGGAC ATTCCCAACA TGCTCACTCC CTTAATCTGT CCGTCTAGAG GTTTGGCTTC 180
30 TACAAACCAA GGGAGTCGAC GAGTTGAAG ATG AAG CCC AGA GCG GAG TGC TGT 233
Met Lys Pro Arg Ala Glu Cys Cys
1 5
35 TCT CCC AAG TTC TGG TTG GTG TTG GCC GTC CTG GCC GTG TCA GGC AGC 281

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	Ser Pro Lys Phe Trp Leu Val Leu Ala Val Leu Ala Val Ser Gly Ser	
	10 15 20	
5	AGA GCT CGT TCT CAG AAG AGC CCC CCC AGC ATT GGC ATT GCT GTC ATC	329
	Arg Ala Arg Ser Gln Lys Ser Pro Pro Ser Ile Gly Ile Ala Val Ile	
	25 30 35 40	
10	CTC GTG GGC ACT TCC GAC GAG GTG GCC ATC AAG GAT GCC CAC GAG AAA	377
	Leu Val Gly Thr Ser Asp Glu Val Ala Ile Lys Asp Ala His Glu Lys	
	45 50 55	
15	GAT GAT TTC CAC CAT CTC TCC GTG GTA CCC CGG GTG GAA CTG GTA GCC	425
	Asp Asp Phe His His Leu Ser Val Val Pro Arg Val Glu Leu Val Ala	
	60 65 70	
20	ATG AAT GAG ACC GAC CCA AAG AGC ATC ATC ACC CGC ATC TGT GAT CTC	473
	Met Asn Glu Thr Asp Pro Lys Ser Ile Ile Thr Arg Ile Cys Asp Leu	
	75 80 85	
25	ATG TCT GAC CGG AAG ATC CAG GGG GTG GTG TTT GCT GAT GAC ACA GAC	521
	Met Ser Asp Arg Lys Ile Gln Gly Val Val Phe Ala Asp Asp Thr Asp	
	90 95 100	
30	CAG GAA GCC ATC GCC CAG ATC CTC GAT TTC ATT TCA GCA CAG ACT CTC	569
	Gln Glu Ala Ile Ala Gln Ile Leu Asp Phe Ile Ser Ala Gln Thr Leu	
	105 110 115 120	
35	ACC CCG ATC CTG GGC ATC CAC GGG GGC TCC TCT ATG ATA ATG GCA GAT	617
	Thr Pro Ile Leu Gly Ile His Gly Gly Ser Ser Met Ile Met Ala Asp	
	125 130 135	
	AAG GAT GAA TCC TCC ATG TTC TTC CAG TTT GGC CCA TCA ATT GAA CAG	665
	Lys Asp Glu Ser Ser Met Phe Phe Gln Phe Gly Pro Ser Ile Glu Gln	
	140 145 150	

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ATT GCC ATA ATC ACC ACT GCT GCT TCT GAC ATG CTG TCT GAG CAC AGC 1145
 Ile Ala Ile Ile Thr Thr Ala Ala Ser Asp Met Leu Ser Glu His Ser
 300 305 310

5

TTC ATC CCT GAG CCC AAA AGC AGT TGT TAC AAC ACC CAC GAG AAG AGA 1193
 Phe Ile Pro Glu Pro Lys Ser Ser Cys Tyr Asn Thr His Glu Lys Arg
 315 320 325

10

ATC TAC CAG TCC AAT ATG CTA AAT AGG TAT CTG ATC AAT GTC ACT TTT 1241
 Ile Tyr Gln Ser Asn Met Leu Asn Arg Tyr Leu Ile Asn Val Thr Phe
 330 335 340

15

GAG GGG AGG AAT TTG TCC TTC AGT GAA GAT GGC TAC CAG ATG CAC CCG 1289
 Glu Gly Arg Asn Leu Ser Phe Ser Glu Asp Gly Tyr Gln Met His Pro
 345 350 355 360

20

AAA CTG GTG ATA ATT CTT CTG AAC AAG GAG AGG AAG TGG GAA AGG GTG 1337
 Lys Leu Val Ile Ile Leu Leu Asn Lys Glu Arg Lys Trp Glu Arg Val
 365 370 375

25

GGG AAG TGG AAA GAC AAG TCC CTG CAG ATG AAG TAC TAT GTG TGG CCC 1385
 Gly Lys Trp Lys Asp Lys Ser Leu Gln Met Lys Tyr Tyr Val Trp Pro
 380 385 390

30

CGA ATG TGT CCA GAG ACT GAA GAG CAG GAG GAT GAC CAT CTG AGC ATT 1433
 Arg Met Cys Pro Glu Thr Glu Glu Gln Glu Asp Asp His Leu Ser Ile
 395 400 405

35

GTG ACC CTG GAG GAG GCA CCA TTT GTC ATT GTG GAA AGT GTG GAC CCT 1481
 Val Thr Leu Glu Glu Ala Pro Phe Val Ile Val Glu Ser Val Asp Pro
 410 415 420

CTG AGT GGA ACC TGC ATG AGG AAC ACA GTC CCC TGC CAA AAA CGC ATA 1529
 Leu Ser Gly Thr Cys Met Arg Asn Thr Val Pro Cys Gln Lys Arg Ile

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	425	430	435	440	
	GTC ACT GAG AAT AAA ACA GAC GAG GAG CCG GGT TAC ATC AAA AAA TGC				1577
	Val Thr Glu Asn Lys Thr Asp Glu Glu Pro Gly Tyr Ile Lys Lys Cys				
5		445	450	455	
	TGC AAG GGG TTC TGT ATT GAC ATC CTT AAG AAA ATT TCT AAA TCT GTG				1625
	Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys Ile Ser Lys Ser Val				
	460	465	470		
10	AAG TTC ACC TAT GAC CTT TAC CTG GTT ACC AAT GGC AAG CAT GGG AAG				1673
	Lys Phe Thr Tyr Asp Leu Tyr Leu Val Thr Asn Gly Lys His Gly Lys				
	475	480	485		
15	AAA ATC AAT GGA ACC TGG AAT GGT ATG ATT GGA GAG GTG GTC ATG AAG				1721
	Lys Ile Asn Gly Thr Trp Asn Gly Met Ile Gly Glu Val Val Met Lys				
	490	495	500		
	AGG GCC TAC ATG GCA GTG GGC TCA CTC ACC ATC AAT GAG GAA CGA TCG				1769
20	Arg Ala Tyr Met Ala Val Gly Ser Leu Thr Ile Asn Glu Glu Arg Ser				
	505	510	515	520	
	GAG GTG GTC GAC TTC TCT GTG CCC TTC ATA GAG ACA GGC ATC AGT GTC				1817
	Glu Val Val Asp Phe Ser Val Pro Phe Ile Glu Thr Gly Ile Ser Val				
25		525	530	535	
	ATG GTG TCA CGC AGC AAT GGG ACT GTC TCA CCT TCT GCC TTC TTA GAG				1865
	Met Val Ser Arg Ser Asn Gly Thr Val Ser Pro Ser Ala Phe Leu Glu				
	540	545	550		
30	CCA TTC AGC GCT GAC GTA TGG GTG ATG ATG TTT GTG ATG CTG CTC ATC				1913
	Pro Phe Ser Ala Asp Val Trp Val Met Met Phe Val Met Leu Leu Ile				
	555	560	565		
35	GTC TCA GCC GTG GCT GTC TTT GTC TTT GAG TAC TTC AGC CCT GTG GGT				1961

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	Val Ser Ala Val Ala Val Phe Val Phe Glu Tyr Phe Ser Pro Val Gly	
	570 575 580	
5	TAT AAC AGG TGC CTC GCT GAT GGC AGA GAG CCT GGT GGA CCC TCT TTC Tyr Asn Arg Cys Leu Ala Asp Gly Arg Glu Pro Gly Gly Pro Ser Phe	2009
	585 590 595 600	
10	ACC ATC GGC AAA GCT ATT TGG TTG CTC TGG GGT CTG GTG TTT AAC AAC Thr Ile Gly Lys Ala Ile Trp Leu Leu Trp Gly Leu Val Phe Asn Asn	2057
	605 610 615	
15	TCC GTA CCT GTG CAG AAC CCA AAG GGG ACC ACC TCC AAG ATC ATG GTG Ser Val Pro Val Gln Asn Pro Lys Gly Thr Thr Ser Lys Ile Met Val	2105
	620 625 630	
20	TCA GTG TGG GCC TTC TTT GCT GTC ATC TTC CTG GCC AGC TAC ACT GCC Ser Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Ser Tyr Thr Ala	2153
	635 640 645	
25	AAC TTA GCT GCC TTC ATG ATC CAA GAG GAA TAT GTG GAC CAG GTT TCT Asn Leu Ala Ala Phe Met Ile Gln Glu Glu Tyr Val Asp Gln Val Ser	2201
	650 655 660	
30	GGC CTG AGC GAC AAA AAG TTC CAG AGA CCT AAT GAC TTC TCA CCC CCT Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Asn Asp Phe Ser Pro Pro	2249
	665 670 675 680	
35	TTC CGC TTT GGG ACC GTG CCC AAC GGC AGC ACA GAG AGA AAT ATT CGC Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Arg Asn Ile Arg	2297
	685 690 695	
40	AAT AAC TAT GCA GAA ATG CAT GCC TAC ATG GGA AAG TTC AAC CAG AGG Asn Asn Tyr Ala Glu Met His Ala Tyr Met Gly Lys Phe Asn Gln Arg	2345
	700 705 710	

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	GGT GTA GAT GAT GCA TTG CTC TCC CTG AAA ACA GGG AAA CTG GAT GCC	2393
	Gly Val Asp Asp Ala Leu Leu Ser Leu Lys Thr Gly Lys Leu Asp Ala	
	715 720 725	
5	TTC ATC TAT GAT GCA GCA GTG CTG AAC TAT ATG GCA GGC AGA GAT GAA	2441
	Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala Gly Arg Asp Glu	
	730 735 740	
	GGC TGC AAG CTG GTG ACC ATT GGC AGT GGG AAG GTC TTT GCT TCC ACT	2489
10	Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe Ala Ser Thr	
	745 750 755 760	
	GGC TAT GGC ATT GCC ATC CAA AAA GAT TCT GGG TGG AAG CGC CAG GTG	2537
	Gly Tyr Gly Ile Ala Ile Gln Lys Asp Ser Gly Trp Lys Arg Gln Val	
15	765 770 775	
	GAC CTT GCT ATC CTG CAG CTC TTT GGA GAT GGG GAG ATG GAA GAA CTG	2585
	Asp Leu Ala Ile Leu Gln Leu Phe Gly Asp Gly Glu Met Glu Glu Leu	
	780 785 790	
20	GAA GCT CTC TGG CTC ACT GGC ATT TGT CAC AAT GAG AAG AAT GAG GTC	2633
	Glu Ala Leu Trp Leu Thr Gly Ile Cys His Asn Glu Lys Asn Glu Val	
	795 800 805	
25	ATG AGC AGC CAG CTG GAC ATT GAC AAC ATG GCA GGG GTC TTC TAC ATG	2681
	Met Ser Ser Gln Leu Asp Ile Asp Asn Met Ala Gly Val Phe Tyr Met	
	810 815 820	
	TTG GGG GCG GCC ATG GCT CTC AGC CTC ATC ACC TTC ATC TGC GAA CAC	2729
30	Leu Gly Ala Ala Met Ala Leu Ser Leu Ile Thr Phe Ile Cys Glu His	
	825 830 835 840	
	CTT TTC TAT TGG CAG TTC CGA CAT TGC TTT ATG GGT GTC TGT TCT GGC	2777
	Leu Phe Tyr Trp Gln Phe Arg His Cys Phe Met Gly Val Cys Ser Gly	
35	845 850 855	

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	AAG CCT GGC ATG GTC TTC TCC ATC AGC AGA GGT ATC TAC AGC TGC ATC	2825
	Lys Pro Gly Met Val Phe Ser Ile Ser Arg Gly Ile Tyr Ser Cys Ile	
	860 865 870	
5		
	CAT GGG GTG GCG ATC GAG GAG CGC CAG TCT GTA ATG AAC TCC CCC ACC	2873
	His Gly Val Ala Ile Glu Glu Arg Gln Ser Val Met Asn Ser Pro Thr	
	875 880 885	
10		
	GCA ACC ATG AAC AAC ACA CAC TCC AAC ATC CTG CGC CTG CTG CGC ACG	2921
	Ala Thr Met Asn Asn Thr His Ser Asn Ile Leu Arg Leu Leu Arg Thr	
	890 895 900	
	GCC AAG AAC ATG GCT AAC CTG TCT GGT GTG AAT GGC TCA CCG CAG AGC	2969
15	Ala Lys Asn Met Ala Asn Leu Ser Gly Val Asn Gly Ser Pro Gln Ser	
	905 910 915 920	
	GCC CTG GAC TTC ATC CGA CGG GAG TCA TCC GTC TAT GAC ATC TCA GAG	3017
	Ala Leu Asp Phe Ile Arg Arg Glu Ser Ser Val Tyr Asp Ile Ser Glu	
20	925 930 935	
	CAC CGC CGC AGC TTC ACG CAT TCT GAC TGC AAA TCC TAC AAC AAC CCG	3065
	His Arg Arg Ser Phe Thr His Ser Asp Cys Lys Ser Tyr Asn Asn Pro	
	940 945 950	
25		
	CCC TGT GAG GAG AAC CTC TTC AGT GAC TAC ATC AGT GAG GTA GAG AGA	3113
	Pro Cys Glu Glu Asn Leu Phe Ser Asp Tyr Ile Ser Glu Val Glu Arg	
	955 960 965	
30		
	ACG TTC GGG AAC CTG CAG CTG AAG GAC AGC AAC GTG TAC CAA GAT CAC	3161
	Thr Phe Gly Asn Leu Gln Leu Lys Asp Ser Asn Val Tyr Gln Asp His	
	970 975 980	
	TAC CAC CAT CAC CAC CGG CCC CAT AGT ATT GGC AGT GCC AGC TCC ATC	3209
35	Tyr His His His His Arg Pro His Ser Ile Gly Ser Ala Ser Ser Ile	

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	985	990	995	1000	
	GAT GGG CTC TAC GAC TGT GAC AAC CCA CCC TTC ACC ACC CAG TCC AGG				3257
	Asp Gly Leu Tyr Asp Cys Asp Asn Pro Pro Phe Thr Thr Gln Ser Arg				
5		1005	1010	1015	
	TCC ATC AGC AAG AAG CCC CTG GAC ATC GGC CTC CCC TCC TCC AAG CAC				3305
	Ser Ile Ser Lys Lys Pro Leu Asp Ile Gly Leu Pro Ser Ser Lys His				
		1020	1025	1030	
10	AGC CAG CTC AGT GAC CTG TAC GGC AAA TTC TCC TTC AAG AGC GAC CGC				3353
	Ser Gln Leu Ser Asp Leu Tyr Gly Lys Phe Ser Phe Lys Ser Asp Arg				
		1035	1040	1045	
15	TAC AGT GGC CAC GAC GAC TTG ATC CGC TCC GAT GTC TCT GAC ATC TCA				3401
	Tyr Ser Gly His Asp Asp Leu Ile Arg Ser Asp Val Ser Asp Ile Ser				
		1050	1055	1060	
	ACC CAC ACC GTC ACC TAT GGG AAC ATC GAG GGC AAT GCC GCC AAG AGG				3449
20	Thr His Thr Val Thr Tyr Gly Asn Ile Glu Gly Asn Ala Ala Lys Arg				
		1065	1070	1075	1080
	CGT AAG CAG CAA TAT AAG GAC AGC CTG AAG AAG CGG CCT GCC TCG GCC				3497
	Arg Lys Gln Gln Tyr Lys Asp Ser Leu Lys Lys Arg Pro Ala Ser Ala				
25		1085	1090	1095	
	AAG TCC CGC AGG GAG TTT GAC GAG ATC GAG CTG GCC TAC CGT CGC CGA				3545
	Lys Ser Arg Arg Glu Phe Asp Glu Ile Glu Leu Ala Tyr Arg Arg Arg				
		1100	1105	1110	
30	CCG CCC CGC TCC CCT GAC CAC AAG CGC TAC TTC AGG GAC AAG GAA GGG				3593
	Pro Pro Arg Ser Pro Asp His Lys Arg Tyr Phe Arg Asp Lys Glu Gly				
		1115	1120	1125	
35	CTA CGG GAC TTC TAC CTG GAC CAG TTC CGA ACA AAG GAG AAC TCA CCC				3641

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	Leu Arg Asp Phe Tyr Leu Asp Gln Phe Arg Thr Lys Glu Asn Ser Pro	
	1130 1135 1140	
5	CAC TGG GAG CAC GTA GAC CTG ACC GAC ATC TAC AAG GAG CGG AGT GAT	3689
	His Trp Glu His Val Asp Leu Thr Asp Ile Tyr Lys Glu Arg Ser Asp	
	1145 1150 1155 1160	
10	GAC TTT AAG CGC GAC TCC ATC AGC GGA GGA GGG CCC TGT ACC AAC AGG	3737
	Asp Phe Lys Arg Asp Ser Ile Ser Gly Gly Gly Pro Cys Thr Asn Arg	
	1165 1170 1175	
15	TCT CAC ATC AAG CAC GGG ACG GGC GAC AAA CAC GGC GTG GTC AGC GGG	3785
	Ser His Ile Lys His Gly Thr Gly Asp Lys His Gly Val Val Ser Gly	
	1180 1185 1190	
	GTA CCT GCA CCT TGG GAG AAG AAC CTG ACC AAC GTG GAG TGG GAG GAC	3833
	Val Pro Ala Pro Trp Glu Lys Asn Leu Thr Asn Val Glu Trp Glu Asp	
	1195 1200 1205	
20	CGG TCC GGG GGC AAC TTC TGC CGC AGC TGT CCC TCC AAG CTG CAC AAC	3881
	Arg Ser Gly Gly Asn Phe Cys Arg Ser Cys Pro Ser Lys Leu His Asn	
	1210 1215 1220	
25	TAC TCC ACG ACG GTG ACG GGT CAG AAC TCG GGC AGG CAG GCG TGC ATC	3929
	Tyr Ser Thr Thr Val Thr Gly Gln Asn Ser Gly Arg Gln Ala Cys Ile	
	1225 1230 1235 1240	
30	CGG TGT GAG GCT TGC AAG AAA GCA GGC AAC CTG TAT GAC ATC AGT GAG	3977
	Arg Cys Glu Ala Cys Lys Lys Ala Gly Asn Leu Tyr Asp Ile Ser Glu	
	1245 1250 1255	
35	GAC AAC TCC CTG CAG GAA CTG GAC CAG CCG GCT GCC CCA GTG GCG GTG	4025
	Asp Asn Ser Leu Gln Glu Leu Asp Gln Pro Ala Ala Pro Val Ala Val	
	1260 1265 1270	

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	ACG TCA AAC GCC TCC ACC ACT AAG TAC CCT CAG AGC CCG ACT AAT TCC	4073
	Thr Ser Asn Ala Ser Thr Thr Lys Tyr Pro Gln Ser Pro Thr Asn Ser	
	1275 1280 1285	
5	AAG GCC CAG AAG AAG AAC CGG AAC AAA CTG CGC CGG CAG CAC TCC TAC	4121
	Lys Ala Gln Lys Lys Asn Arg Asn Lys Leu Arg Arg Gln His Ser Tyr	
	1290 1295 1300	
10	GAC ACC TTC GTG GAC CTG CAG AAG GAA GAA GCC GCC CTG GCC CCG CGC	4169
	Asp Thr Phe Val Asp Leu Gln Lys Glu Glu Ala Ala Leu Ala Pro Arg	
	1305 1310 1315 1320	
15	AGC GTA AGC CTG AAA GAC AAG GGC CGA TTC ATG GAT GGG AGC CCC TAC	4217
	Ser Val Ser Leu Lys Asp Lys Gly Arg Phe Met Asp Gly Ser Pro Tyr	
	1325 1330 1335	
20	GCC CAC ATG TTT GAG ATG TCA GCT GGC GAG AGC ACC TTT GCC AAC AAC	4265
	Ala His Met Phe Glu Met Ser Ala Gly Glu Ser Thr Phe Ala Asn Asn	
	1340 1345 1350	
	AAG TCC TCA GTG CCC ACT GCC GGA CAT CAC CAC CAC AAC AAC CCC GGC	4313
	Lys Ser Ser Val Pro Thr Ala Gly His His His His Asn Asn Pro Gly	
	1355 1360 1365	
25	GGC GGG TAC ATG CTC AGC AAG TCG CTC TAC CCT GAC CGG GTC ACG CAA	4361
	Gly Gly Tyr Met Leu Ser Lys Ser Leu Tyr Pro Asp Arg Val Thr Gln	
	1370 1375 1380	
30	AAC CCT TTC ATC CCC ACT TTT GGG GAC GAC CAG TGC TTG CTC CAT GGC	4409
	Asn Pro Phe Ile Pro Thr Phe Gly Asp Asp Gln Cys Leu Leu His Gly	
	1385 1390 1395 1400	
35	AGC AAA TCC TAC TTC TTC AGG CAG CCC ACG GTG GCG GGG GCG TCG AAA	4457
	Ser Lys Ser Tyr Phe Phe Arg Gln Pro Thr Val Ala Gly Ala Ser Lys	
	1405 1410 1415	

	GCC AGG CCG GAC TTC CGG GCC CTT GTC ACC AAC AAG CCG GTG GTC TCG	4505
	Ala Arg Pro Asp Phe Arg Ala Leu Val Thr Asn Lys Pro Val Val Ser	
	1420 1425 1430	
5		
	GCC CTT CAT GGG GCC GTG CCA GCC CGT TTC CAG AAG GAC ATC TGT ATA	4553
	Ala Leu His Gly Ala Val Pro Ala Arg Phe Gln Lys Asp Ile Cys Ile	
	1435 1440 1445	
10		
	GGG AAC CAG TCC AAC CCC TGT GTG CCT AAC AAC ACA AAC CCC AGG GCT	4601
	Gly Asn Gln Ser Asn Pro Cys Val Pro Asn Asn Thr Asn Pro Arg Ala	
	1450 1455 1460	
	TTC AAT GGC TCC AGC AAT GGG CAT GTT TAT GAG AAA CTT TCT AGT ATT	4649
15	Phe Asn Gly Ser Ser Asn Gly His Val Tyr Glu Lys Leu Ser Ser Ile	
	1465 1470 1475 1480	
	GAG TCT GAT GTC TGAGTGAGGG AACAGAGAGG TTAAGGTGGG TACGGGAGGG	4701
	Glu Ser Asp Val	
20	148	
	TAAGGCTGTG GGTGCGGTGA TGCGCATGTC ACGGAGGGTG ACGGGGGTGA ACTTGGTTC	4761
	CATTTGCTCC TTTCTTGTTT TAATTTATTT ATGGGATCCT GGAGTTCTGG TTCCTACTGG	4821
25		
	GGGCAACCCT GGTGACCAGC ACCATCTCTC CTCCTTTTCA CAGTTCTCTC CTTCTTCCCC	4881
	CCGCTGTCAG CCATTCCTGT TCCCATGAGA TGATGCCATG GGCCCTCTCA GCAGGGGAGG	4941
30	GTAGAGCGGA GAAAGGAAGG GCTGCATGCG GGCTTCCTCC TGGTGTGGAA GAGCTCCTTG	5001
	ATATCCTCTT TGAGTGAAGC TGGGAGAACC AAAAAGAGGC TATGTGAGCA CAAAGGTAGC	5061
	TTTTCCTAAA CTGATCTTTT CATTTAGGTG AGGAAGCAA AGCATCTATG TGAGACCATT	5121
35		

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5181 TAGCACACTG CTTGTGAAAG GAAAGAGGCT CTGGCTAAAT TCATGCTGCT TAGATGACAT

5241 CTGTCTAGGA ATCATGTGCC AAGCAGAGGT TGGGAGGCCA TTTGTGTTTA TATATAAGCC

5 5301 CAAAAATGCT TGCTTCAACC CCATGAGACT CGATAGTGGT GGTGAACAGA ACCCAAGGTC

5361 ATTGGTGGCA GAGTGGATTC TTGAACAAAC TGGAAAGTAC GTTATGATAG TGTCCCCCGG

5421 TGCCTTGGGG ACAAGAGCAG GTGGATTGTG CGTGCATGTG TGTTCATGCA CACTTGCACC

10 5481 CATGTGTAGT CAGGTGCCTC AAGAGAAGGC AACCTTGACT CTTTCGTTGA ATTTGCATCT

5538 CTTCAAGACA CAAGATTAAA ACAAATTTA CGCTAAATTG GATTTTAAAT TATCTTC

15

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 1484 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Lys Pro Arg Ala Glu Cys Cys Ser Pro Lys Phe Trp Leu Val Leu

1 5 10 15

30

Ala Val Leu Ala Val Ser Gly Ser Arg Ala Arg Ser Gln Lys Ser Pro

20 25 30

Pro Ser Ile Gly Ile Ala Val Ile Leu Val Gly Thr Ser Asp Glu Val

35 40 45

35

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	Ala	Ile	Lys	Asp	Ala	His	Glu	Lys	Asp	Asp	Phe	His	His	Leu	Ser	Val
	50							55						60		
5	Val	Pro	Arg	Val	Glu	Leu	Val	Ala	Met	Asn	Glu	Thr	Asp	Pro	Lys	Ser
	65					70					75					80
	Ile	Ile	Thr	Arg	Ile	Cys	Asp	Leu	Met	Ser	Asp	Arg	Lys	Ile	Gln	Gly
					85					90					95	
10	Val	Val	Phe	Ala	Asp	Asp	Thr	Asp	Gln	Glu	Ala	Ile	Ala	Gln	Ile	Leu
				100					105					110		
	Asp	Phe	Ile	Ser	Ala	Gln	Thr	Leu	Thr	Pro	Ile	Leu	Gly	Ile	His	Gly
				115				120					125			
15	Gly	Ser	Ser	Met	Ile	Met	Ala	Asp	Lys	Asp	Glu	Ser	Ser	Met	Phe	Phe
	130						135				140					
	Gln	Phe	Gly	Pro	Ser	Ile	Glu	Gln	Gln	Ala	Ser	Val	Met	Leu	Asn	Ile
20	145					150					155					160
	Met	Glu	Glu	Tyr	Asp	Trp	Tyr	Ile	Phe	Ser	Ile	Val	Thr	Thr	Tyr	Phe
					165					170					175	
25	Pro	Gly	Tyr	Gln	Asp	Phe	Val	Asn	Lys	Ile	Arg	Ser	Thr	Ile	Glu	Asn
				180					185					190		
	Ser	Phe	Val	Gly	Trp	Glu	Leu	Glu	Glu	Val	Leu	Leu	Leu	Asp	Met	Ser
			195					200					205			
30	Leu	Asp	Asp	Gly	Asp	Ser	Lys	Ile	Gln	Asn	Gln	Leu	Lys	Lys	Leu	Gln
	210						215					220				
	Ser	Pro	Ile	Ile	Leu	Leu	Tyr	Cys	Thr	Lys	Glu	Glu	Ala	Thr	Tyr	Ile
35	225					230					235					240

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	Phe	Glu	Val	Ala	Asn	Ser	Val	Gly	Leu	Thr	Gly	Tyr	Gly	Tyr	Thr	Trp	
					245					250						255	
5	Ile	Val	Pro	Ser	Leu	Val	Ala	Gly	Asp	Thr	Asp	Thr	Val	Pro	Ala	Glu	
					260					265						270	
	Phe	Pro	Thr	Gly	Leu	Ile	Ser	Val	Ser	Tyr	Asp	Glu	Trp	Asp	Tyr	Gly	
					275					280						285	
10	Leu	Pro	Pro	Arg	Val	Arg	Asp	Gly	Ile	Ala	Ile	Ile	Thr	Thr	Ala	Ala	
					290					295						300	
	Ser	Asp	Met	Leu	Ser	Glu	His	Ser	Phe	Ile	Pro	Glu	Pro	Lys	Ser	Ser	
15	305						310						315			320	
	Cys	Tyr	Asn	Thr	His	Glu	Lys	Arg	Ile	Tyr	Gln	Ser	Asn	Met	Leu	Asn	
							325						330			335	
20	Arg	Tyr	Leu	Ile	Asn	Val	Thr	Phe	Glu	Gly	Arg	Asn	Leu	Ser	Phe	Ser	
						340						345				350	
	Glu	Asp	Gly	Tyr	Gln	Met	His	Pro	Lys	Leu	Val	Ile	Ile	Leu	Leu	Asn	
						355						360				365	
25	Lys	Glu	Arg	Lys	Trp	Glu	Arg	Val	Gly	Lys	Trp	Lys	Asp	Lys	Ser	Leu	
						370						375				380	
	Gln	Met	Lys	Tyr	Tyr	Val	Trp	Pro	Arg	Met	Cys	Pro	Glu	Thr	Glu	Glu	
30	385						390					395				400	
	Gln	Glu	Asp	Asp	His	Leu	Ser	Ile	Val	Thr	Leu	Glu	Glu	Ala	Pro	Phe	
						405						410				415	
35	Val	Ile	Val	Glu	Ser	Val	Asp	Pro	Leu	Ser	Gly	Thr	Cys	Met	Arg	Asn	

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	420	425	430
	Thr Val Pro Cys Gln Lys Arg Ile Val Thr Glu Asn Lys Thr Asp Glu		
	435	440	445
5	Glu Pro Gly Tyr Ile Lys Lys Cys Cys Lys Gly Phe Cys Ile Asp Ile		
	450	455	460
	Leu Lys Lys Ile Ser Lys Ser Val Lys Phe Thr Tyr Asp Leu Tyr Leu		
10	465	470	475 480
	Val Thr Asn Gly Lys His Gly Lys Lys Ile Asn Gly Thr Trp Asn Gly		
	485	490	495
15	Met Ile Gly Glu Val Val Met Lys Arg Ala Tyr Met Ala Val Gly Ser		
	500	505	510
	Leu Thr Ile Asn Glu Glu Arg Ser Glu Val Val Asp Phe Ser Val Pro		
	515	520	525
20	Phe Ile Glu Thr Gly Ile Ser Val Met Val Ser Arg Ser Asn Gly Thr		
	530	535	540
	Val Ser Pro Ser Ala Phe Leu Glu Pro Phe Ser Ala Asp Val Trp Val		
25	545	550	555 560
	Met Met Phe Val Met Leu Leu Ile Val Ser Ala Val Ala Val Phe Val		
	565	570	575
30	Phe Glu Tyr Phe Ser Pro Val Gly Tyr Asn Arg Cys Leu Ala Asp Gly		
	580	585	590
	Arg Glu Pro Gly Gly Pro Ser Phe Thr Ile Gly Lys Ala Ile Trp Leu		
	595	600	605
35			

Leu Trp Gly Leu Val Phe Asn Asn Ser Val Pro Val Gln Asn Pro Lys
 610 615 620
 Gly Thr Thr Ser Lys Ile Met Val Ser Val Trp Ala Phe Phe Ala Val
 5 625 630 635 640
 Ile Phe Leu Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln
 645 650 655
 10 Glu Glu Tyr Val Asp Gln Val Ser Gly Leu Ser Asp Lys Lys Phe Gln
 660 665 670
 Arg Pro Asn Asp Phe Ser Pro Pro Phe Arg Phe Gly Thr Val Pro Asn
 675 680 685
 15 Gly Ser Thr Glu Arg Asn Ile Arg Asn Asn Tyr Ala Glu Met His Ala
 690 695 700
 Tyr Met Gly Lys Phe Asn Gln Arg Gly Val Asp Asp Ala Leu Leu Ser
 20 705 710 715 720
 Leu Lys Thr Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu
 725 730 735
 25 Asn Tyr Met Ala Gly Arg Asp Glu Gly Cys Lys Leu Val Thr Ile Gly
 740 745 750
 Ser Gly Lys Val Phe Ala Ser Thr Gly Tyr Gly Ile Ala Ile Gln Lys
 755 760 765
 30 Asp Ser Gly Trp Lys Arg Gln Val Asp Leu Ala Ile Leu Gln Leu Phe
 770 775 780
 Gly Asp Gly Glu Met Glu Glu Leu Glu Ala Leu Trp Leu Thr Gly Ile
 35 785 790 795 800

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	Cys His Asn Glu Lys Asn Glu Val Met Ser Ser Gln Leu Asp Ile Asp	
	805	810 815
5	Asn Met Ala Gly Val Phe Tyr Met Leu Gly Ala Ala Met Ala Leu Ser	
	820	825 830
	Leu Ile Thr Phe Ile Cys Glu His Leu Phe Tyr Trp Gln Phe Arg His	
	835	840 845
10	Cys Phe Met Gly Val Cys Ser Gly Lys Pro Gly Met Val Phe Ser Ile	
	850	855 860
	Ser Arg Gly Ile Tyr Ser Cys Ile His Gly Val Ala Ile Glu Glu Arg	
15	865	870 875 880
	Gln Ser Val Met Asn Ser Pro Thr Ala Thr Met Asn Asn Thr His Ser	
	885	890 895
20	Asn Ile Leu Arg Leu Leu Arg Thr Ala Lys Asn Met Ala Asn Leu Ser	
	900	905 910
	Gly Val Asn Gly Ser Pro Gln Ser Ala Leu Asp Phe Ile Arg Arg Glu	
	915	920 925
25	Ser Ser Val Tyr Asp Ile Ser Glu His Arg Arg Ser Phe Thr His Ser	
	930	935 940
	Asp Cys Lys Ser Tyr Asn Asn Pro Pro Cys Glu Glu Asn Leu Phe Ser	
30	945	950 955 960
	Asp Tyr Ile Ser Glu Val Glu Arg Thr Phe Gly Asn Leu Gln Leu Lys	
	965	970 975
35	Asp Ser Asn Val Tyr Gln Asp His Tyr His His His His Arg Pro His	

980 985 990
 Ser Ile Gly Ser Ala Ser Ser Ile Asp Gly Leu Tyr Asp Cys Asp Asn
 995 1000 1005
 5
 Pro Pro Phe Thr Thr Gln Ser Arg Ser Ile Ser Lys Lys Pro Leu Asp
 1010 1015 1020
 Ile Gly Leu Pro Ser Ser Lys His Ser Gln Leu Ser Asp Leu Tyr Gly
 10 1025 1030 1035 1040
 Lys Phe Ser Phe Lys Ser Asp Arg Tyr Ser Gly His Asp Asp Leu Ile
 1045 1050 1055
 15 Arg Ser Asp Val Ser Asp Ile Ser Thr His Thr Val Thr Tyr Gly Asn
 1060 1065 1070
 Ile Glu Gly Asn Ala Ala Lys Arg Arg Lys Gln Gln Tyr Lys Asp Ser
 1075 1080 1085
 20 Leu Lys Lys Arg Pro Ala Ser Ala Lys Ser Arg Arg Glu Phe Asp Glu
 1090 1095 1100
 Ile Glu Leu Ala Tyr Arg Arg Arg Pro Pro Arg Ser Pro Asp His Lys
 25 1105 1110 1115 1120
 Arg Tyr Phe Arg Asp Lys Glu Gly Leu Arg Asp Phe Tyr Leu Asp Gln
 1125 1130 1135
 30 Phe Arg Thr Lys Glu Asn Ser Pro His Trp Glu His Val Asp Leu Thr
 1140 1145 1150
 Asp Ile Tyr Lys Glu Arg Ser Asp Asp Phe Lys Arg Asp Ser Ile Ser
 1155 1160 1165
 35

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	Gly Gly Gly Pro Cys Thr Asn Arg Ser His Ile Lys His Gly Thr Gly	
	1170	1175 1180
5	Asp Lys His Gly Val Val Ser Gly Val Pro Ala Pro Trp Glu Lys Asn	
	1185	1190 1195 1200
	Leu Thr Asn Val Glu Trp Glu Asp Arg Ser Gly Gly Asn Phe Cys Arg	
	1205	1210 1215
10	Ser Cys Pro Ser Lys Leu His Asn Tyr Ser Thr Thr Val Thr Gly Gln	
	1220	1225 1230
	Asn Ser Gly Arg Gln Ala Cys Ile Arg Cys Glu Ala Cys Lys Lys Ala	
	1235	1240 1245
15	Gly Asn Leu Tyr Asp Ile Ser Glu Asp Asn Ser Leu Gln Glu Leu Asp	
	1250	1255 1260
	Gln Pro Ala Ala Pro Val Ala Val Thr Ser Asn Ala Ser Thr Thr Lys	
20	1265	1270 1275 1280
	Tyr Pro Gln Ser Pro Thr Asn Ser Lys Ala Gln Lys Lys Asn Arg Asn	
	1285	1290 1295
25	Lys Leu Arg Arg Gln His Ser Tyr Asp Thr Phe Val Asp Leu Gln Lys	
	1300	1305 1310
	Glu Glu Ala Ala Leu Ala Pro Arg Ser Val Ser Leu Lys Asp Lys Gly	
	1315	1320 1325
30	Arg Phe Met Asp Gly Ser Pro Tyr Ala His Met Phe Glu Met Ser Ala	
	1330	1335 1340
	Gly Glu Ser Thr Phe Ala Asn Asn Lys Ser Ser Val Pro Thr Ala Gly	
35	1345	1350 1355 1360

His His His His Asn Asn Pro Gly Gly Tyr Met Leu Ser Lys Ser
1365 1370 1375

5 Leu Tyr Pro Asp Arg Val Thr Gln Asn Pro Phe Ile Pro Thr Phe Gly
1380 1385 1390

Asp Asp Gln Cys Leu Leu His Gly Ser Lys Ser Tyr Phe Phe Arg Gln
1395 1400 1405

10 Pro Thr Val Ala Gly Ala Ser Lys Ala Arg Pro Asp Phe Arg Ala Leu
1410 1415 1420

Val Thr Asn Lys Pro Val Val Ser Ala Leu His Gly Ala Val Pro Ala
15 1425 1430 1435 1440

Arg Phe Gln Lys Asp Ile Cys Ile Gly Asn Gln Ser Asn Pro Cys Val
1445 1450 1455

20 Pro Asn Asn Thr Asn Pro Arg Ala Phe Asn Gly Ser Ser Asn Gly His
1460 1465 1470

Val Tyr Glu Lys Leu Ser Ser Ile Glu Ser Asp Val
1475 1480

25

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- 30 (A) LENGTH: 4695 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both
- 35 (ii) MOLECULE TYPE: cDNA

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(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 485..4495

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

	CGAGAACACA GCGAGTGTGT GAGTCCCTCC CGCTCCAGCT CCTCCAAGCC GCGGCCGCCG	60
10	CCGCCACCCT CGCCCGCAGC CTCCCGCAGC CTCCCTCGGC CACCGGTGTC TGGTGGGGGT	120
	GTGCTCTGGG TAGGTCGGCC CGGCCCCCAG GGGTCTCTCG AGCGTCTGCC ATCTGCCCGA	180
	GAAACATGTG TGGCCACGTC CTCGCCTAGT CCAGGTGGCC GCAACCTTGG GGGAGAGACA	240
15	GGGCAGGACA GGACCAAGGT AAGAGGTAAG GAGGAGACGG CGCCAGGGAC AGACAGGAGG	300
	TCCCGGCTTG CCGTTGTGCG CACCACCACT GCCGCCGCC CGGGGCCTGC CCCCACATC	360
20	GGCTCTCTGA GCCCTCCTCG GAATCTTGGG GTCGCTGGAC GCCGGGTTCC GGTCTTGCC	420
	CCCCCGCCAT CCCCCAACA GAACAGGGTC ATGAAAAGAG GCCGCCCGGC GGGGCCCGCA	480
	GGCG ATG CGC GGC GCC GGT GGC CCC CGC GGC CCT CGG GGC CCC GCT AAG	529
25	Met Arg Gly Ala Gly Gly Pro Arg Gly Pro Arg Gly Pro Ala Lys	
	1 5 10 15	
	ATG CTG CTG CTG CTG GCG CTG GCC TGC GCC AGC CCG TTC CCG GAG GAG	577
	Met Leu Leu Leu Leu Ala Leu Ala Cys Ala Ser Pro Phe Pro Glu Glu	
30	20 25 30	
	GCG CCG GGG CCG GGC GGG GCC GGT GGG CCC GGC GGC GGC CTC GGC GGG	625
	Ala Pro Gly Pro Gly Gly Ala Gly Gly Pro Gly Gly Gly Leu Gly Gly	
	35 40 45	

35

	GCG CGG CCG CTC AAC GTG GCG CTC GTG TTC TCG GGG CCC GCG TAC GCG	673
	Ala Arg Pro Leu Asn Val Ala Leu Val Phe Ser Gly Pro Ala Tyr Ala	
	50 55 60	
5	GCC GAG GCG GCA CGC CTG GGC CCG GCC GTG GCG GCG GCG GTG CGC AGC	721
	Ala Glu Ala Ala Arg Leu Gly Pro Ala Val Ala Ala Ala Val Arg Ser	
	65 70 75	
	CCG GGC CTA GAC GTG CGG CCC GTG GCG CTG GTG CTC AAC GGC TCG GAC	769
10	Pro Gly Leu Asp Val Arg Pro Val Ala Leu Val Leu Asn Gly Ser Asp	
	80 85 90 95	
	CCG CGC AGC CTC GTG CTG CAG CTC TGC GAC CTG CTG TCG GGG TTG CGC	817
15	Pro Arg Ser Leu Val Leu Gln Leu Cys Asp Leu Leu Ser Gly Leu Arg	
	100 105 110	
	GTG CAC GGC GTG GTC TTC GAA GAC GAC TCG CGC GCG CCC GCC GTC GCG	865
20	Val His Gly Val Val Phe Glu Asp Asp Ser Arg Ala Pro Ala Val Ala	
	115 120 125	
	CCC ATC CTC GAC TTC CTG TCG GCG CAG ACC TCG CTC CCC ATC GTG TCC	913
25	Pro Ile Leu Asp Phe Leu Ser Ala Gln Thr Ser Leu Pro Ile Val Ser	
	130 135 140	
	GAG CAC GGC GGC GCC GCG CTC GTG CTC ACG CCC AAG GAG AAG GGC TCC	961
30	Glu His Gly Gly Ala Ala Leu Val Leu Thr Pro Lys Glu Lys Gly Ser	
	145 150 155	
	ACC TTC CTC CAC CTG GGC TCT TCC CCC GAG CAA CAG CTT CAG GTC ATC	1009
35	Thr Phe Leu His Leu Gly Ser Ser Pro Glu Gln Gln Leu Gln Val Ile	
	160 165 170 175	
	TTT GAG GTG CTG GAG GAG TAT GAC TGG ACG TCC TTT GTA GCC GTG ACC	1057
	Phe Glu Val Leu Glu Glu Tyr Asp Trp Thr Ser Phe Val Ala Val Thr	
	180 185 190	

ACT CGT GCC CCT GGC CAC CGG GCC TTC CTG TCC TAC ATT GAG GTG CTG 1105
 Thr Arg Ala Pro Gly His Arg Ala Phe Leu Ser Tyr Ile Glu Val Leu
 195 200 205

5

ACT GAC GGC AGT CTG GTG GGC TGG GAG CAC CGC GGA GCG CTG ACG CTG 1153
 Thr Asp Gly Ser Leu Val Gly Trp Glu His Arg Gly Ala Leu Thr Leu
 210 215 220

10

GAC CCT GGG GCG GGC GAG GCC GTG CTC AGT GCC CAG CTC CGC AGT GTC 1201
 Asp Pro Gly Ala Gly Glu Ala Val Leu Ser Ala Gln Leu Arg Ser Val
 225 230 235

15

AGC GCG CAG ATC CGC CTG CTC TTC TGC GCC CGA GAG GAG GCC GAG CCC 1249
 Ser Ala Gln Ile Arg Leu Leu Phe Cys Ala Arg Glu Glu Ala Glu Pro
 240 245 250 255

20

GTG TTC CGC GCA GCT GAG GAG GCT GGC CTC ACT GGA TCT GGC TAC GTC 1297
 Val Phe Arg Ala Ala Glu Glu Ala Gly Leu Thr Gly Ser Gly Tyr Val
 260 265 270

25

TGG TTC ATG GTG GGG CCC CAG CTG GCT GGA GGC GGG GGC TCT GGG GCC 1345
 Trp Phe Met Val Gly Pro Gln Leu Ala Gly Gly Gly Gly Ser Gly Ala
 275 280 285

30

CCT GGT GAG CCC CCT CTT CTG CCA GGA GGC GCC CCC CTG CCT GCC GGG 1393
 Pro Gly Glu Pro Pro Leu Leu Pro Gly Gly Ala Pro Leu Pro Ala Gly
 290 295 300

35

CTG TTT GCA GTG CGC TCG GCT GGC TGG CGG GAT GAC CTG GCT CGG CGA 1441
 Leu Phe Ala Val Arg Ser Ala Gly Trp Arg Asp Asp Leu Ala Arg Arg
 305 310 315

GTG GCA GCT GGC GTG GCC GTA GTG GCC AGA GGT GCC CAG GCC CTG CTG 1489
 Val Ala Ala Gly Val Ala Val Val Ala Arg Gly Ala Gln Ala Leu Leu

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	Ser Gln Leu Asn Arg Thr His Ser Pro Pro Pro Asp Ala Pro Arg Pro	
	465 470 475	
5	GAA AAG CGC TGC TGC AAG GGT TTC TGC ATC GAC ATT CTG AAG CGG CTG Glu Lys Arg Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Arg Leu	1969
	480 485 490 495	
10	GCG CAT ACC ATC GGC TTC AGC TAC GAC CTC TAC CTG GTC ACC AAT GGC Ala His Thr Ile Gly Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn Gly	2017
	500 505 510	
15	AAG CAC GGA AAG AAG ATC GAT GGC GTC TGG AAC GGC ATG ATC GGG GAG Lys His Gly Lys Lys Ile Asp Gly Val Trp Asn Gly Met Ile Gly Glu	2065
	515 520 525	
20	GTG TTC TAC CAG CGC GCA GAC ATG GCC ATC GGC TCC CTC ACC ATC AAC Val Phe Tyr Gln Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile Asn	2113
	530 535 540	
25	GAG GAG CGC TCC GAG ATC GTG GAC TTC TCC GTC CCC TTC GTG GAG ACC Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu Thr	2161
	545 550 555	
30	GGC ATC AGC GTC ATG GTG GCG CGC AGC AAT GGC ACG GTG TCC CCC TCG Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro Ser	2209
	560 565 570 575	
35	GCC TTC CTC GAG CCC TAC AGC CCC GCC GTG TGG GTG ATG ATG TTC GTC Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe Val	2257
	580 585 590	
	ATG TGC CTC ACT GTG GTC GCC GTC ACT GTT TTC ATC TTC GAG TAC CTC Met Cys Leu Thr Val Val Ala Val Thr Val Phe Ile Phe Glu Tyr Leu	2305
	595 600 605	

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	AGT CCT GTT GGT TAC AAC CGC AGC CTG GCC ACG GGC AAG CGC CCT GGC	2353
	Ser Pro Val Gly Tyr Asn Arg Ser Leu Ala Thr Gly Lys Arg Pro Gly	
	610 615 620	
5	GGT TCA ACC TTC ACC ATT GGG AAA TCC ATC TGG CTG CTC TGG GCC CTG	2401
	Gly Ser Thr Phe Thr Ile Gly Lys Ser Ile Trp Leu Leu Trp Ala Leu	
	625 630 635	
10	GTG TTC AAT AAT TCG GTG CCC GTG GAG AAC CCC CGG GGA ACC ACC AGC	2449
	Val Phe Asn Asn Ser Val Pro Val Glu Asn Pro Arg Gly Thr Thr Ser	
	640 645 650 655	
15	AAA ATC ATG GTG CTG GTG TGG GCC TTC TTC GCC GTC ATC TTC CTC GCC	2497
	Lys Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala	
	660 665 670	
20	AGC TAC ACA GCC AAC CTG GCC GCC TTC ATG ATC CAG GAG GAG TAC GTG	2545
	Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Glu Tyr Val	
	675 680 685	
25	GAT ACT GTG TCT GGG CTC AGT GAC CGC AAG TTC CAG AGG CCC CAG GAG	2593
	Asp Thr Val Ser Gly Leu Ser Asp Arg Lys Phe Gln Arg Pro Gln Glu	
	690 695 700	
30	CAG TAC CCG CCC CTG AAG TTT GGG ACC GTG CCC AAC GGC TCC ACG GAG	2641
	Gln Tyr Pro Pro Leu Lys Phe Gly Thr Val Pro Asn Gly Ser Thr Glu	
	705 710 715	
35	AAG AAC ATC CGC AGC AAC TAT CCC GAC ATG CAC AGC TAC ATG GTG CGC	2689
	Lys Asn Ile Arg Ser Asn Tyr Pro Asp Met His Ser Tyr Met Val Arg	
	720 725 730 735	
40	TAC AAC CAG CCC CGC GTA GAG GAA GCG CTC ACT CAG CTC AAG GCA GGG	2737
	Tyr Asn Gln Pro Arg Val Glu Glu Ala Leu Thr Gln Leu Lys Ala Gly	
	740 745 750	

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	880	885	890	895	
	TGC TGC AGC GCT GAG GCC GCC CCA CCG CCC GCC AAG CCC CCG CCG CCG				3217
	Cys Cys Ser Ala Glu Ala Ala Pro Pro Pro Ala Lys Pro Pro Pro Pro				
5		900	905	910	
	CCA CAG CCC CTG CCC AGC CCC GCG TAC CCC GCG CCG GGG CCG GCT CCC				3265
	Pro Gln Pro Leu Pro Ser Pro Ala Tyr Pro Ala Pro Gly Pro Ala Pro				
		915	920	925	
10					
	GGG CCC GCA CCT TTC GTC CCC CGC GAG CGC GCC TCA GTG GCC CGC TGG				3313
	Gly Pro Ala Pro Phe Val Pro Arg Glu Arg Ala Ser Val Ala Arg Trp				
		930	935	940	
15					
	CGC CGG CCC AAG GGC GCG GGG CCG CCG GGG GGC GCG GGC CTG GCC GAC				3361
	Arg Arg Pro Lys Gly Ala Gly Pro Pro Gly Gly Ala Gly Leu Ala Asp				
		945	950	955	
	GGC TTC CAC CGC TAC TAC GGC CCC ATC GAG CCG CAG GGC CTA GGC CTC				3409
20					
	Gly Phe His Arg Tyr Tyr Gly Pro Ile Glu Pro Gln Gly Leu Gly Leu				
		960	965	970	975
	GGC CTG GGC GAA GCG CGC GCG GCA CCG CGG GGC GCA GCC GGG CGC CCG				3457
	Gly Leu Gly Glu Ala Arg Ala Ala Pro Arg Gly Ala Ala Gly Arg Pro				
25		980	985	990	
	CTG TCC CCG CCG GCC GCT CAG CCC CCG CAG AAG CCG CCG GCC TCC TAT				3505
	Leu Ser Pro Pro Ala Ala Gln Pro Pro Gln Lys Pro Pro Ala Ser Tyr				
		995	1000	1005	
30					
	TTC GCC ATC GTA CGC GAC AAG GAG CCA GCC GAG CCC CCC GCC GGC GCC				3553
	Phe Ala Ile Val Arg Asp Lys Glu Pro Ala Glu Pro Pro Ala Gly Ala				
		1010	1015	1020	
35					
	TTC CCC GGC TTC CCG TCC CCG CCC GCG CCC CCC GCC GCC GCG GCC ACC				3601

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	Phe Pro Gly Phe Pro Ser Pro Pro Ala Pro Pro Ala Ala Ala Ala Thr	
	1025 1030 1035	
5	GCC GTC GGG CCG CCA CTC TGC CGC TTG GCC TTC GAG GAC GAG AGC CCG Ala Val Gly Pro Pro Leu Cys Arg Leu Ala Phe Glu Asp Glu Ser Pro	3649
	1040 1045 1050 1055	
10	CCG GCG CCC GCG CGG TGG CCG CGC TCG GAC CCC GAG AGC CAA CCC CTG Pro Ala Pro Ala Arg Trp Pro Arg Ser Asp Pro Glu Ser Gln Pro Leu	3697
	1060 1065 1070	
15	CTG GGG CCA GGC GCG GGC GGC GCG GGG GGC ACG GGG GGC GCA GGC GGA Leu Gly Pro Gly Ala Gly Gly Ala Gly Gly Thr Gly Gly Ala Gly Gly	3745
	1075 1080 1085	
	GGA GCC CCG GCC GCT CCG CCC CCG TGC TTC GCC GCG CCG CCC CCG TGC Gly Ala Pro Ala Ala Pro Pro Pro Cys Phe Ala Ala Pro Pro Pro Cys	3793
	1090 1095 1100	
20	TTT TAC CTC GAT GTC GAC CAG TCG CCG TCG GAC TCG GAG GAC TCG GAG Phe Tyr Leu Asp Val Asp Gln Ser Pro Ser Asp Ser Glu Asp Ser Glu	3841
	1105 1110 1115	
25	AGC CTG GCC GGC GCG TCC CTG GCC GGC CTG GAT CCC TGG TGG TTC GCC Ser Leu Ala Gly Ala Ser Leu Ala Gly Leu Asp Pro Trp Trp Phe Ala	3889
	1120 1125 1130 1135	
30	GAC TTC CCT TAC CCG TAT GCC GAT CGC CTC GGG CSG CCC GCG GCA CGC Asp Phe Pro Tyr Pro Tyr Ala Asp Arg Leu Gly Xaa Pro Ala Ala Arg	3937
	1140 1145 1150	
35	TAC GGA TTG GTC GAC AAA CTA GGG GGC TGG CTC GCC GGG AGC TGG GAC Tyr Gly Leu Val Asp Lys Leu Gly Gly Trp Leu Ala Gly Ser Trp Asp	3985
	1155 1160 1165	

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	TAC CTG CCT CCS CGC AGC GGT CGG GCC GCC TGG CAC TGT CGG CAC TGC	4033
	Tyr Leu Pro Xaa Arg Ser Gly Arg Ala Ala Trp His Cys Arg His Cys	
	1170 1175 1180	
5	GCC AGC CTG GAG CTG CTT CCG CCG CCG CGC CAT CTC AGC TGC TCG CAC	4081
	Ala Ser Leu Glu Leu Leu Pro Pro Pro Arg His Leu Ser Cys Ser His	
	1185 1190 1195	
10	GAT GGC CTG GAC GGC GGC TGG TGG GCG CCA CCG CCT CCA CCC TGG GCC	4129
	Asp Gly Leu Asp Gly Gly Trp Trp Ala Pro Pro Pro Pro Pro Trp Ala	
	1200 1205 1210 1215	
15	GCC GGG CCC CTG CCC CGA CGC CGG GCC CGC TGC GGG TGC CCG CGG TCG	4177
	Ala Gly Pro Leu Pro Arg Arg Arg Ala Arg Cys Gly Cys Pro Arg Ser	
	1220 1225 1230	
20	CAC CCG CAC CGC CCG CGG GCC TCG CAC CGC ACG CCC GCC GCT GCC GCG	4225
	His Pro His Arg Pro Arg Ala Ser His Arg Thr Pro Ala Ala Ala Ala	
	1235 1240 1245	
25	CCC CAC CAC CAC AGG CAC CGG CGC GCC GCT GGG GGC TGG GAC CTC CCG	4273
	Pro His His His Arg His Arg Arg Ala Ala Gly Gly Trp Asp Leu Pro	
	1250 1255 1260	
30	CCG CCC GCG CCC ACC TCG CGC TCG CTC GAG GAC CTC AGC TCG TGC CCT	4321
	Pro Pro Ala Pro Thr Ser Arg Ser Leu Glu Asp Leu Ser Ser Cys Pro	
	1265 1270 1275	
35	CGC GCC GCC CCT GCG CGC AGG CTT ACC GGG CCC TCC CGC CAC GCT CGC	4369
	Arg Ala Ala Pro Ala Arg Arg Leu Thr Gly Pro Ser Arg His Ala Arg	
	1280 1285 1290 1295	
40	AGG TGT CCG CAC GCC GCG CAC TGG GGG CCG CCG CTG CCT ACA GCT TCC	4417
	Arg Cys Pro His Ala Ala His Trp Gly Pro Pro Leu Pro Thr Ala Ser	
	1300 1305 1310	

	CAC CGG AGA CAC CGG GGC GGG GAC CTG GGC ACC CGC AGG GGC TCG GCG	4465
	His Arg Arg His Arg Gly Gly Asp Leu Gly Thr Arg Arg Gly Ser Ala	
	1315 1320 1325	
5		
	CAC TTC TCT AGC CTC GAG TCC GAG GTA TGACGCGGCC CCGGGGGCCC	4512
	His Phe Ser Ser Leu Glu Ser Glu Val	
	1330 1335	
10		
	CACCGCCCCC TTGGTCAGCG CAGGCCACGG CCCGAGGGGG CGCCCGCAGT GGACAGGACC	4572
	CGCGTGGGT'T GGGAAGGAAA GCAGTGGAAC TGGCCGGACC CCGCCTGGAG CAGCGTCCTG	4632
	CGCCCCCTGG TTCTGGAGGA ACCGCAAGCC GGAGAGGATT TGGTCCCTCA ACTATCACCC	4692
15		
	AGG	4695

(2) INFORMATION FOR SEQ ID NO:16:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1336 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

30 Met Arg Gly Ala Gly Gly Pro Arg Gly Pro Arg Gly Pro Ala Lys Met
1 5 10 15
Leu Leu Leu Leu Ala Leu Ala Cys Ala Ser Pro Phe Pro Glu Glu Ala
20 25 30

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Pro Gly Pro Gly Gly Ala Gly Gly Pro Gly Gly Gly Leu Gly Gly Ala
35 40 45

Arg Pro Leu Asn Val Ala Leu Val Phe Ser Gly Pro Ala Tyr Ala Ala
5 50 55 60

Glu Ala Ala Arg Leu Gly Pro Ala Val Ala Ala Ala Val Arg Ser Pro
65 70 75 80

Gly Leu Asp Val Arg Pro Val Ala Leu Val Leu Asn Gly Ser Asp Pro
85 90 95

Arg Ser Leu Val Leu Gln Leu Cys Asp Leu Leu Ser Gly Leu Arg Val
100 105 110

His Gly Val Val Phe Glu Asp Asp Ser Arg Ala Pro Ala Val Ala Pro
115 120 125

Ile Leu Asp Phe Leu Ser Ala Gln Thr Ser Leu Pro Ile Val Ser Glu
130 135 140

His Gly Gly Ala Ala Leu Val Leu Thr Pro Lys Glu Lys Gly Ser Thr
145 150 155 160

Phe Leu His Leu Gly Ser Ser Pro Glu Gln Gln Leu Gln Val Ile Phe
165 170 175

Glu Val Leu Glu Glu Tyr Asp Trp Thr Ser Phe Val Ala Val Thr Thr
180 185 190

Arg Ala Pro Gly His Arg Ala Phe Leu Ser Tyr Ile Glu Val Leu Thr
195 200 205

Asp Gly Ser Leu Val Gly Trp Glu His Arg Gly Ala Leu Thr Leu Asp
210 215 220

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	Pro Gly Ala Gly Glu Ala Val Leu Ser Ala Gln Leu Arg Ser Val Ser	
	225	230 235 240
5	Ala Gln Ile Arg Leu Leu Phe Cys Ala Arg Glu Glu Ala Glu Pro Val	
	245	250 255
	Phe Arg Ala Ala Glu Glu Ala Gly Leu Thr Gly Ser Gly Tyr Val Trp	
	260	265 270
10	Phe Met Val Gly Pro Gln Leu Ala Gly Gly Gly Gly Ser Gly Ala Pro	
	275	280 285
	Gly Glu Pro Pro Leu Leu Pro Gly Gly Ala Pro Leu Pro Ala Gly Leu	
15	290	295 300
	Phe Ala Val Arg Ser Ala Gly Trp Arg Asp Asp Leu Ala Arg Arg Val	
	305	310 315 320
20	Ala Ala Gly Val Ala Val Val Ala Arg Gly Ala Gln Ala Leu Leu Arg	
	325	330 335
	Asp Tyr Gly Phe Leu Pro Glu Leu Gly His Asp Cys Arg Ala Gln Asn	
	340	345 350
25	Arg Thr His Arg Gly Glu Ser Leu His Arg Tyr Phe Met Asn Ile Thr	
	355	360 365
	Trp Asp Asn Arg Asp Tyr Ser Phe Asn Glu Asp Gly Phe Leu Val Asn	
30	370	375 380
	Pro Ser Leu Val Val Ile Ser Leu Thr Arg Asp Arg Thr Trp Glu Val	
	385	390 395 400
35	Val Gly Ser Trp Glu Gln Gln Thr Leu Arg Leu Lys Tyr Pro Leu Trp	

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	405	410	415
	Ser Arg Tyr Gly Arg Phe Leu Gln Pro Val Asp Asp Thr Gln His Leu		
	420	425	430
5	Ala Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val Glu Pro Ala		
	435	440	445
	Asp Pro Ile Ser Gly Thr Cys Ile Arg Asp Ser Val Pro Cys Arg Ser		
10	450	455	460
	Gln Leu Asn Arg Thr His Ser Pro Pro Pro Asp Ala Pro Arg Pro Glu		
	465	470	475 480
15	Lys Arg Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Arg Leu Ala		
	485	490	495
	His Thr Ile Gly Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn Gly Lys		
	500	505	510
20	His Gly Lys Lys Ile Asp Gly Val Trp Asn Gly Met Ile Gly Glu Val		
	515	520	525
	Phe Tyr Gln Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile Asn Glu		
25	530	535	540
	Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu Thr Gly		
	545	550	555 560
30	Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro Ser Ala		
	565	570	575
	Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe Val Met		
	580	585	590
35			

Cys Leu Thr Val Val Ala Val Thr Val Phe Ile Phe Glu Tyr Leu Ser
 595 600 605
 Pro Val Gly Tyr Asn Arg Ser Leu Ala Thr Gly Lys Arg Pro Gly Gly
 5 610 615 620
 Ser Thr Phe Thr Ile Gly Lys Ser Ile Trp Leu Leu Trp Ala Leu Val
 625 630 635 640
 10 Phe Asn Asn Ser Val Pro Val Glu Asn Pro Arg Gly Thr Thr Ser Lys
 645 650 655
 Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Ser
 660 665 670
 15 Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Glu Tyr Val Asp
 675 680 685
 Thr Val Ser Gly Leu Ser Asp Arg Lys Phe Gln Arg Pro Gln Glu Gln
 20 690 695 700
 Tyr Pro Pro Leu Lys Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Lys
 705 710 715 720
 25 Asn Ile Arg Ser Asn Tyr Pro Asp Met His Ser Tyr Met Val Arg Tyr
 725 730 735
 Asn Gln Pro Arg Val Glu Glu Ala Leu Thr Gln Leu Lys Ala Gly Lys
 740 745 750
 30 Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala Arg
 755 760 765
 Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe
 35 770 775 780

Ala Thr Thr Gly Tyr Gly Ile Ala Leu His Lys Gly Ser Arg Trp Lys
785 790 795 800

5 Arg Pro Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Asp Glu Ile
805 810 815

Glu Met Leu Glu Arg Leu Trp Leu Ser Gly Ile Cys His Asn Asp Lys
820 825 830

10 Ile Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Ala Gly Val
835 840 845

Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ser Leu Leu Val Phe Ala
15 850 855 860

Trp Glu His Leu Val Tyr Trp Arg Leu Arg His Cys Leu Gly Pro Thr
865 870 875 880

20 His Arg Met Asp Phe Leu Leu Ala Phe Ser Arg Gly Met Tyr Ser Cys
885 890 895

Cys Ser Ala Glu Ala Ala Pro Pro Pro Ala Lys Pro Pro Pro Pro Pro
900 905 910

25 Gln Pro Leu Pro Ser Pro Ala Tyr Pro Ala Pro Gly Pro Ala Pro Gly
915 920 925

Pro Ala Pro Phe Val Pro Arg Glu Arg Ala Ser Val Ala Arg Trp Arg
30 930 935 940

Arg Pro Lys Gly Ala Gly Pro Pro Gly Gly Ala Gly Leu Ala Asp Gly
945 950 955 960

35 Phe His Arg Tyr Tyr Gly Pro Ile Glu Pro Gln Gly Leu Gly Leu Gly

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	Gly Leu Val Asp Lys Leu Gly Gly Trp Leu Ala Gly Ser Trp Asp Tyr
	1155 1160 1165
5	Leu Pro Xaa Arg Ser Gly Arg Ala Ala Trp His Cys Arg His Cys Ala
	1170 1175 1180
	Ser Leu Glu Leu Leu Pro Pro Pro Arg His Leu Ser Cys Ser His Asp
	1185 1190 1195 1200
10	Gly Leu Asp Gly Gly Trp Trp Ala Pro Pro Pro Pro Pro Trp Ala Ala
	1205 1210 1215
	Gly Pro Leu Pro Arg Arg Arg Ala Arg Cys Gly Cys Pro Arg Ser His
	1220 1225 1230
15	Pro His Arg Pro Arg Ala Ser His Arg Thr Pro Ala Ala Ala Ala Pro
	1235 1240 1245
	His His His Arg His Arg Arg Ala Ala Gly Gly Trp Asp Leu Pro Pro
20	1250 1255 1260
	Pro Ala Pro Thr Ser Arg Ser Leu Glu Asp Leu Ser Ser Cys Pro Arg
	1265 1270 1275 1280
25	Ala Ala Pro Ala Arg Arg Leu Thr Gly Pro Ser Arg His Ala Arg Arg
	1285 1290 1295
	Cys Pro His Ala Ala His Trp Gly Pro Pro Leu Pro Thr Ala Ser His
	1300 1305 1310
30	Arg Arg His Arg Gly Gly Asp Leu Gly Thr Arg Arg Gly Ser Ala His
	1315 1320 1325
	Phe Ser Ser Leu Glu Ser Glu Val
35	1330 1335

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(2) INFORMATION FOR SEQ ID NO:17:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

10

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

15

GGGTGGCGGC CGCAGAGCAC CTCCACCATC TCCTTGCCT ACTCCAAGAT CTGGCCCTAG 60

TCCATGTTTG C 71

20

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 base pairs

(B) TYPE: nucleic acid

25

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGGTGGTCCC CAACCTGTAG GACTTGGTTC TGGAGGAGGA TCTGGTGTAG GCAAACATGG 60

ACTAGGGCCA G 71

35

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

10 (ii) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:19:

15 GTTGGGGACC ACCAGATGGA GGTAGAGCTG CACTTGTACG AAGAGCTCCA CAACCACCTG 60
G 61

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
25 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:20:

30 CGTGAGACGT CAGACAAAGG AGGCCAGGT GTAGGTGGTC TACCAGGTGG TTGTGGAGCT 60
CT 62

35

(i) SEQUENCE CHARACTERISTICS:

5

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

10

15

TAGAGCTGCA CTTGTACGAA GAGCTCCACA ACCACCTGGT AGACCACCTA CACCTGGGCC 180

20